

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCGTCTCGGAGAC
 TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
 TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
 TCATTATTCTTTTGGGCACCTTTGGTTGTTTGTCTACCTGCCGAGCTTCTGCATGGATGCTA
 AAAGTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTTCGAACTGGTTCGCTGCCATCGTAGG
 ATTTGTTTTTTCAGACATGAGATTAAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
 TGTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
 TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
 ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
 ATTTCCCTTTGGAGTTGCTTGCTTCCAACGATTGGAATCTTCTCGCCTACTGCCWCTCTCG
 TGCCATAACAAATAACCAGTATGAGATAGT**GTA**ACCAATGTATCTGTGGCCTATTCCCTCT
 CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
 ACAACACTACTTACTGATAGACCAAAAACTACACCAAGTGGTTGATTCAATCAAGATGTAT
 GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGAGTGGGCTGAT
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTTCATGTTAGATCG
 TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

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FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTIVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

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FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGTAGGCTCTGGAAGGGGCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
 GTTCCCTCTTTCCGGGGTCCCTACCAGAAGAGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAAATCC
 TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAACTACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGTGTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGGCTAGTGTTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTTCGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGCGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGCTTGCTGTCTACTTTGCTGTGAAATGTCTAAATGTTTC
 TGTCAGAGAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEIHAF LGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTTGGCC
 CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGACTG
 CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
 CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCCTTCTGCTTTTCCGAAGC
 CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC
 CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
 CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTCTCCTGAGCCTTACGCTGGCCACTGTCAAC
 GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
 GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
 GAGAGAAGGACCCCAAGTACAGTGTCTCTCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
 TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCCTTGCCCTGGA
 AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
 AAAAAAAAAA

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FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFTRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

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FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGAATTTTCATGAAC TAGCAAGAGGACACCATCTT
 CTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
 AGAATTTTGATAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTCCCGGCGTCTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAGATGCCAAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCAAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTTGGATTGCAAAAGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG
 CTCAGTTTTCTTTGAAAAGGAGGCTGGAATGTTACATACATAGGCAAGTCTGCCCTGT
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
 ATCTTTACCGTGGCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTT
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 AAAAAAAAAAAAAAAAAA

1006768.120601

FIGURE 8

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ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATGG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCGTGCACCACCT
 GTAGTCATGTACCCACGCGCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTGCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCCTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAAACCAGCAAAATCCACCCCTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCCTGTGGATCCCCGCCCGAAGGAG
 ATCCGACAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCCACCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCCAACAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA
 AAGGATACCCCAAGTTTTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTTGGAGACAGCATCCGCATCCTGGGGGGGCTCCTGAGTGCCTTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTTCAGAACACCTTCCAAAGTTTCTTACTCGGATGTGAACATCGGTACTGGGATGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCGGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGGA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
 AGCCATCGAGGGGTGCAGAACGCACCTGCTGCGGCACCTCCGAGCCAGTAAGCTCAACCTTG
 TGGGGGAGCTTGCCACGCGCCGCTTCAGTGCCAAAGATGGACCACCTGGTGTGCTTCTCGCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCAGGA
 GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCATTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCTCACAGGGGA
 CCGCAAATACCAGGACTTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC
 CCTCGGTTGGCTATTCTCCATCAACAATGTCCAGGATCTCAGAGCCCGAGCCTTAGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
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 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGGACAGGCACTTGTG
 CTGGTCTGTGGCATTTCGAAGGGCCACGTAGCACCGGCAACGCCAAGTGGCCAGGCT
 CTGAAGTGGCTTGGGCTCTCTCGTCTCTGCTTTAATCAGGACACCGTGGAGACAAGTGA
 GGCCGTGAGTCTTGGGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTGCTTCTCTC
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCGGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGTGACCGAGTGCAGGACCGGAGGTCGAGC
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FIGURE 10

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><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
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SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLSEEQMRPE
IAGLKPANPFVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAWEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTfVGE LAHGRFS AKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATGT**TCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCTGCCCCCAGAG
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CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTTCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
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GCCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG
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CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGACATTC
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100676.12601

FIGURE 12

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 GQGQETSGFPACFPPEPPPEHWEEDASWGPHRLAVLPFRERFEELLVFVPHMRRFLSRKKI
 RHIIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVLLPLNEELDYGFEAGPFHVA
 SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
 TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
 NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

1006768.120601

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTCATTAAGAAATTGTTCCCTTCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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109021-8290001

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
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PRGEGEKVGDG

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

10006768.120601

FIGURE 15

GGGACCCATCGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCGCCGCCGGGGGAGGCCCGCTCCTCCGGCCGCCATAGGCTCCGGTTCGCCGCTGG
 CGCCGCGCCGCGCTCCTGCCGCCGGGCTCCGGGCGGCCGTAGGCCAGTCGCCGCCGCC
 CTCGCCCCGAGGCCCGGCCGCCGAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCCGGCGGC
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 GCATCGCTGGGTAAAGGAGAAGACATACGGTACGGGATACAGGTTGTTTATCCTAAGT
 CACTGCAGGCCCAACAGTCAAGCGCTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATTGCCGCTCTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACGCTT
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 ATGTTCTCGATTGTTGGGAGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAAATACATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTTCTACAGT**TAA**ATTAGAATGCTCCAATGTTCTGCTTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTTGAGGAGATAGGTATTATTGCTTTTGTCTACTGTTTAAAGAAAACATA
 ACCAGGAAGAACTGCATTACGACTTTCAGGGCCCTAGGCATTTTTGCTTTTGATTCCCTTT
 CTTACATAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATACT
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 TTGAAGCAGCAAAAATGAAAGCATTTTACTGATTTTTTAAATTGGTGCTTTAGATATATTT
 GACTACAGTGATTTGAAGCAAATAGAGGAGGCACAACCTCAGCAACCTAATGGAACCATTT
 TTTTTCACTTAGCTTTCTGTGGCATGTGAATTGTATTCTCTGCGGTTTTTAATCTCACAG
 TACTTTATTCTGTCTGTGCCCTCAATAATATCACAACAATATTCAGTCATTTTAAATGGC
 TGCATAAATCTGATCCAACAGGTGTTAGGTGTCTGTTTAGTGTGAGCCTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAAAA

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FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPDPTLPNRTVTLLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNLSGNLFSSLSQGTFDYLASLRSLFQTF
EYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELELPsfymTP
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRITGLSDYGRDPENGLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

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FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGTGGGCCTCTCGGTGCTGCTGACGGCGGCC
 ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
 CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
 TTTTGACTGAGCAACTGAAGCAGAAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA
 TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
 GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCTTTTAAACTTGATCA
 AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
 GTGTGGGCAGACACTTTTGGAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
 TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
 TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
 TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

1006768-120601

FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

1006768-100601

FIGURE 19

CTGTCGTCTTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCC**ATG**CCAGTGACGGTAACCCGACCACCATCACAAACCACACGACGTATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTCACTGGTGTCTTCGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCCTCTTCTGCCTCTCGGGCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTGTCCACGGGCCGTTTCGGGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGGCCCGGCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGTGAAGTGCTGGAGACCTTCGTTCGCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCTGCTGAACCTGGGG
 GAGTGCACCAAGTGCTACCATCCCCCTCCCGAGCTTCTGTGCGGGGTGGCCTTGCTGTG
 TGTCTCTCTATGCCACCGCCCTTGTTCCTGCGCCCTCTACCAGTTTCATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGACTCTGCCACCTGGTTTTTGTCAAGGCT**TAA**GACTCTCCCAAGAGGCTCC
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTTCTGTGTTTTCTCTTCTGCTCTCCCTCCCTCCACCTTTTCTTTCTTCTCC
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTCTCTTGTGCTGT
 TTCCTTCCTGTGTGTTTTGTGCCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCACTCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAGCGATTCTCCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTCCTGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACCCCTTGACCGCTCCATGCCACAGCCCC
 CCAAGGGGCCCATTTGCCAAAGCATGCCCTGCCACCCTCGCTGTGCGCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCTTTAAATTAATAAATATATATATATATAT
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCAGCCTGGGTCCCTAGG
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTTGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

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FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLASASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAVTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPAALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPPPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFEVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

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[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRVRQGSVEPESDCSQTVSPDTLCSSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

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FIGURE 23

GGTTCTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT
 GGCACCTCTCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCCTTTCAGACAGGACAACCTGTGATATTTAGTTCTCTGATTGTAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTGCCACATCAAGGGATTGTATTCTTTAAAAAACCATAACCAAAG
 AAGCCTACA**ATG**TTGGCCTTAGCCAAAATCTGTTGATTTCACGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
 TTAAACAAATGGAATAAACCTATTTCTTTGGAAAGTGAGCAAACCTAAACTCAGATAAA
 GAAATATAAACCCCTCAAATCTCAAGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGAGTCTAA
 AACCCACATCTACCATTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCT
 TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA
 ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCACTTCTCCATCTGTGACCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAACAACCTACAGCCTACCTTAAATTCACCAATAATTCAAAACCTCTTTCCAA
 ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGGAAAAAGGAAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
 ATGACCCGGAACCTTATGATGTGAGTTTTGGGAATCTAGCTACTACAATCCAACCTTTGAAT
 GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**AGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTATCTA
 CATCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTCACGTGGAT
 TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGAGACAGGATGTATCAT
 CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
 TCACCATACAGCCCTGCCTCATAACTAAATAATAAAAATTTATCCACCAAAAATTCATAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAGCTGACCCACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTCTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAACCTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSSENF TWSLVNDIVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLF PNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGILLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSVFGNSSYYNP TLNDSA
MPESEENARDGIPMDDIPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

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FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACC GCGC
 AGCCCGAAGATTCACT**ATGTG**GAAAAATCGCCTTCAATACCCCTACCGCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTACAACTACT
 TCATGCCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATGTGTGCTGTCCCCAGTTTCTCTGATAGTGACCTGCGAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCTTCGTGCGAGAGACCTCTTGCTGGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCACTTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAACTACTAACCACTGCAAGCTCTTGTCAAATTTTAGTTTAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC
 GTTGTTTTTTTGTTGTTGTTGTTTTCTTTCCTTTAAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTTGTTTTGAACTTTTTGTGTAAATATATA
 TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTGCAGTTCGTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
 CCTATAATAAATTTTACTCTATACAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRLRRRLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCAGGTGCCCCCCACTCTCGCTCCATTGCGGGGAGCACCAGTCTGTACGCC
 AAGGAAGTGGTCTTGGGGGCACCA**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCGAGCCTCC
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGCCGTGCTCAGGGGTCTTTG
 AGGGGGCTGTGGTGGCCGGTGAAGGCCAAGGGGAGCTGGAAGGGTCTCTCTTTAGCCAG
 GAAGCCCAGGGACCAAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG
 TGT**CTAAC**AGTCTCTCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCTCCTGTGG
 TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTACAGC
 ACAGCTCCCTGACAAAGTGAAGGAGGGCAGCTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACACTACTTTTAAACAA
 GCTACAGGGTAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCAAGCACCCCGGCCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCTGTCTGGCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTCGTCACTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAAATAAACCTTTATTCCGGCCTGAAAAAAAAAA
 AAAGA

1006766.120601

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPGVPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

1006758.120601

FIGURE 29

GTGGACTCTGAGAAGCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCTTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATG
 AAGTTCCAGGGGCCCCCTGGCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGAGGCCCTTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAAGAGGCCGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA
 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG
 AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
 GTCTGGGGACTCCGTGGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
 CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC
 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA
 TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGACATAAACC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTACAGGCTTCA
 GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGGA
 GGCTCTGGAGACAATTATCTGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTAACTCTGAGACGTCTCCTGGGATGTTAACTTTGACACTTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
 AGCTCTCGCATCCCGTGA CCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
 CCCTCCTTAAACACCAACCCTCTCATCTACTAATCTCAGCCCTTGCCCTTGAATAAACCTTA
 GCTGCCCCACAA
 AA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSWSGSGGGDAVGGVNTVNSETPGFMFNFTFWKNFKSKLGFINWDAINKQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

10066768.120601

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGCGGTGCTCACC
 TGCCTCGGTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCTTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCTGCTGCGCTGCACCGGAGCTTGGTGTGTCGAGGAGAGTGAGGGGAAATGATGTGTTCTGCACCAAGC
 TGCTGCTACTTGTGCTCTCGGCTGGCTTTTCCAGATTCCCAAGTCCCTGAGGACTTGTCTTTCTGGAAAGAGG
 GTCCCTCATATGCTCTTGGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAAATGCGCCTGTGGTGGACACAGC
 AGCTGCTCTAGACTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTGCTTCTGTGGGTGTGAGGAGTAGTG
 GACGGATGGGGGCTTCATGAGGAAAATCACCCACCACTACCAAGCTGGGAGGCCAGCCTTCCAGACCA
 GCGAGGGGCTCGAGGACAGCTCGCCCGAGCCTTTTCCACAAACAGCCGCGCTCTCTGCGCGCGAGCTAGAGT
 TCGTGGCAGAAAGAAATGATCAAGCTGTGTCAACATATCAAGCTACACTGGTGCGAGATCTGGTGGCGCAGG
 CAGAGTCACTTCTCCAGAGCAGCTGGTGACACAGGGAGAGGAGGGGAGACCCAGCCAGCTGTGTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGCGGGAGTCTGTCTCAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGAGCCGTTCTGAGCAGTGCAGAGAACATGCTGTGGGG
 TTGCAACAGAGAAAGCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGAGGTGAAAGCAGCAG
 TGAGTCGACACTTCGAGCCAGGGTCTGAACTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAC
 GTGCTCTCTTTGGCGGTGGGGCCACGGGACCTGACAGGGAGTCTCCCAAGAGCATCTGGAACAGCTCTTAGGC
 CAGCTGGGCGAGACGCTGCGGTGCCGCACTTCTGTGCCCACTGCTGAGCAGCATCTGGCAAGTGTCTGTGT
 GAGTTAGCTTCCCTCTCTGTCAGATCAAATTCCTATCTAGSGCCCCGGGACAGTACAGCTGAGGAGAGG
 CAGCTCGAAAGCTTCTGCACATGCTGCTTCTCTTGTGGAAGGAAGACTTTCAGGGGCGGTTCGCTCTTCTGCTA
 TGCTGAGGCCAAGAAATGTGGGGCTTCTGGCAGACACAGGCCAAGGAGTGGGACTTGTCTATTCTTGTCTA
 CGGGAGCTGCTGGAAGAGGTCTGATGGGACGATGGAGATAGAGGCTGCTGCGGACAGCTCCAGCAGGCCAG
 TGCCCTAAGGCTTGTGAGTGGTGACGCCAAACCGGGGACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTTGGGCATTGACCCAGAACCTTGGACCCCGCCTCACGAGGAGGCCAAGTGGCCAAATGCAGACCTTAC
 TGTGTTGGGGTGTAGTGTGCTTACAGTCAAGTCTCTGCTCTAAGGGTGTCACTGGCTGGCAATCCACACCGGA
 ATCTAGAGGAAGAGAGTTGGCTGATTTGGGATTATGGCAGAAAGTCCAGAGATGCACAGTCTTGGATAGAA
 GAGTGTGTTTGTATTCTCTTGGATACATAAATGAAATGAGTGTGTGGGCTTCTCAACAGAGATTCAGGCTCT
 CATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGAATTCATGACAGAGCAATGACTCTGCTTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTTATCACAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCATAACACAGGCGGGTCTGGTGGCTCATGCCTGTAATCCAGCAGCTTGTAGAGGCTGAGGTGCGCG
 GACTGCTGAGTGCAGGAATTCAAGACCAGCTTGGCCAACTGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGCTGGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTGCACTGAGCCGAGGTGCGACCACTGCATCCAGTCTGGGTACAGAGCCGAGACTTCTAG
 AAAAAAGCTTAAACAAAGATAAGTAGGACTCAACCACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCTG
 TGCAGTAGTAACCTCTTGAGACCTCTCCTGACCAGGGACCAAGCAGGAGCAATTAGAGCTTTTATAGAATAAA
 CTGGTTTTCTTAAAAAAGGGCTTTTATTAATAATTCCTCCACACAGTGGCTCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAGGCCCTGTTTTCCTGAGCGGGGCTGGGCTTGTCCATGGTTCGCGGAGCTG
 GCGGTCTGGCGCCCTGGCTGTGTCTAGCTGCTTCTTGGCGGACAGAGCTGCGGGGTCTGGGGCACCGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCTGTCTTAAACCAGACCTGAGGTGCTCCTGAGATCTG
 GTTCACCTGAGTGGCAGGGGAGCAGCTGTGGCCGTGCTCCTTCTAGCGGAGTCTGGGGAACCTAAGCTC
 GGCCCTCTTTTGCAGAACCGAGGATGGGGTGGTGTGGGGACTCATGGGGAATGGCTGAGGAGCTACGTGT
 GAAGAGGGCGCCGTTTGTGGCTGCAGCGGCTCTCTCCTGAGGCTCAGTTTCCCTTCCGTCTA
 ATGAAGAACCTGCGCTCTCGTGTCTCAGGCTATTAGACTTGCCTCAGGAAGTGGCCCTGGAGGAGCTCAT
 GTTATTTTTCAACATGTCTCGACCTTGGCTGGGCACTCATGGAATGGCCATGTGCTCTGTCTGGTGGAC
 GTGCGGCTGGGATGCGGACAGAGGGCGGGGCGAGCTGCGCTGGGGGTGAGGGAGGCGCCCGGAGGG
 CCTCAGGAAGTTGGGCTCCGCAACACAGGACGGCGGGCTCCGCGCGCGCCGCGCACCGCTCCAGG
 GGCGGTAGACAAATGGAATGCGGCTTGGCTCGCTGCGCAGCAGTAGCCCTGTATGCAGTGCGGACGCGG
 TCGTCCGACAGTGAAGCAGCGCCGCTCCACAGCACGAACAGCCGCTGCGCCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQQLAQAFFHNQPP
SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

1006768-120601

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCTCTGCAGCTTCTCTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAAATG
 AGTAGCAACAAGAGCAGCGGTGAGCAGTGTTCTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTG
 GCCGCCGACCTGTCAACCTCAAGAAAGTGAGCATCACTGACGGCTATGTGCCATTCTCGGC
 AACAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT
 GGGCACCAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCCTGGCTACTCAGCTGATGTGGGCAACAAGACCCTACCCGCTCGTGGGCCATTCC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCGAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCGAGGGCAGCCTCGTGCCTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGCCGCATGCGG
 CAATTTGACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGGTGT
 GAGCAGAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCACAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTGAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGTTTCAAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCCCTGCCAAGGAGCTGGGAACTTGGTGTG
 CCCCTCAATTTCCAGCACCAGAAAAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAAATTTGTGGGGTGTGGAGGTTGTGGGGCGGTGGGAGGTCCAGAGGTTGGGA
 GGCTGGCATCCAGGCTTGGCTCTGCCCTGAGACCTTGGAACAAACCTTCCCCCTCTCTGGG
 CACCTTCTGCCACACCAGTTTCCAGTGCGGAGTCTGAGACCTTTCCACCTCCCTACAA
 GTGCCCTCGGGTCTGTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGTGGAAGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCACTCCTTGAAACCTTAAAGGTATTTTGC
 GCAAACTCCTTCAGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT
 CTAGCAGGAGGATTTTCCAAGTGTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTCCGAGGGTCTCCTCGACCTCTGTGCTCTGGGATGGCTGTCTGGGAGCTGT
 ATCACCITGGGTTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAGCTGGGCTCAGTGG
 GGTGTGTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAAGGAGGAGCTGTGA
 GGCTGGAGGGACCATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGTGACTGCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

10006768.120501

FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFRVLRRPQEFVNRTPETVFIFWGPSPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELC DHVHVYGMVPPNYCSQRPRLQRMPIH
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

10006768.120601

FIGURE 35

GTTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGGAAAGCATCCCTAGCTGTTTGGCGCAGAGGGGCGAGGGCTGAAGCCGAGTGGCCCGAGGTTGCTGAGGGGGCTGG
 GCGAAAGGTGAAAGCTTCTCAGAACAGCTTCTGGAAACCCATGACCCATGAAGCTCTTGCCGACATTTATACCGT
 CTGAGGTAGCAGCTCGAAACTAGAGAACTGCACTGTGCCAGGAGCGCAGTATCTCTTCTCTGACCCCTGG
 GGCCATATGGGACCTTGGCTTCAGACCTTTTGATACACCACTGCTGCTGGGAGCACTGACGGCGTTCAGGCGAATG
 AGGCCTGAGGTCAACATGCTTGGCTTCCCTCTCTAGCCACAGCAGGCTGCTTTGCTGACTGAACGAGGTCCCTCAG
 GTCAACCTCCAGCCTCGCTCCACCGCTCCAGAAAGCGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCTCATCAAC
 CACGGGACCCCTGCTCATCATCTGCCCTTAACAACACACACTGTGGGACGGTACAGGTGTGTGGCCCGGATGCTTGGCT
 GGGGCTGTGGCCAGCGTGTGCCAGCACTGTGACACTAGCCATCTCCAGGACTTCAAGTTAGATGTGCAGCAGCTG
 ATTGAAGTGGATAGGGGAAACACGAGCTCATGTGCTGCCACCTGCCTGAGAGCCACCCAAAGGCCAGGTCCGG
 TACAGCTCAAAACAAGAGTGGCTGGAGGCCCTCCAGAGGTAACATACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACAGCTACAACCCAGTGAACCCAGGAAGTGAAGAAC
 TCCGGTCCAGCGCAGGCTACGTGTGCGCCGCTCCACCGCTGAGGTCGCCCGCATCTATCCCCAGAGGGGCC
 CAACACCATCATCGTCAACAAAGGCCAGAGTCTCATTTGGAAGTGTGTGGCCAGTGGAAATCCCAACCCCAACCGGGCT
 CCTTGGGCCAAGGATGGGTCCAGTGTCAACCGCTACAACAAGACGCGCTTCTCTGTGAGCAACCTCCTCATCGAC
 ACCACCGCAGGAGGAGCTCAGGCACTACCGCTGCATGGCCGACAATGGGGTTGGGAGCCCGGGGCGAGGCTG
 ATCCTCTACAATGTCCAGTGTGTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGTGTCATCCCTCGGGG
 CAGAGTGGCCAGCTTACCTGTAGGTGCTGTGGAAACCCCGCCCTCGGTGCTGTGGCTGAGGAATGCTGTGCCCT
 CTATCTCCAGCGCCCTCGCGCTTCCCAAGGCGCTGCGCTGCTCAGCATGGGGCTGAGGACGAGGG
 GTCTACCACTGCTATGCCGAGAAAGCGGTTGGAGCGCCCATGCTGATGGCCCTCGAGCAGCTTCCAGCCGACG
 ATAAACCCCAAGCTGTGGCAGATGCTGAGCTGGCTACTGGCACACTCTCTGTATCACTTCCAACTCCGAGCAC
 CTTAGCAGCATGCTGAGGGGGCAACCGCGCTCCCAAGCCCAACGCTGATGGGGCTGCTTCCCGGAAGTGT
 CCGAGGAGAGAGGGGACGGGGGCTCCCGCGAGGCTCCCATCTCTCAGTGTGCCCGCACCTTCCAAAGACAG
 TCAATATGAAGTGTGTGGCGCTCGGCATGAGGCGAGTGGCGGGCCCAATCTCTACTATGTGTGTAAGAACAC
 CGCAAGCAGGTGCACAAATTCCTCTGACGATGGACCATCTCTGGCATTCAGCAACAGCAGCCGCTGACCTCT
 ACCAGCTTACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAATCTGGGGGAGAGGGGCCAGACAGCC
 ATGGTCACTTCCGAATGGACGGCGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGAGATCCAGAGAGAC
 GACCTTGGAGCCAGTCCCGCAGCAGCAGCCAGCCAGCCAGCGGCCCTCCCGCCCAAGGCTCCCGACAGG
 CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTCCCAATC
 CAGTCTTCCGTGTGGAGTACAAGAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCGGAAGCTCCCGCA
 TCGCGCTGTCGCTGGAGATCAGGSGCTAGAGAAAGGCACTCTTACAAGTTTCCAGTGTCCGGCTCTGAAAGAT
 CTGGGGGAGCGCAGTCCAGCGCCCTCTCGGCCCTACGTTGGTCTGGGCTACAGCGGTGCGCTGTAGGAGAGG
 CCCGTGGCAGTCTTATATCATCTCAGGATGGCTCAATGAGACCATCATGCTCAAGTGGATGTACATC
 CCAGACAGTAAACAACAAACCCCAATCCATGCTTTTATATCTTTATCTTATCCACCAACAGACTGACAAATGAT
 GACTACAAGAAGGATATGGTGAAGGGGCAAGTACTGGCACTCCATCAGCACCTCGAGCCAGAGACCTCTAC
 GCAATTAAGATCAGTGTCTCAATGAAGGAGGGGAGAGCAGTTCAGACAAGCTGATGATCTGTGAGACCAAGCT
 ATAGAAGTCTTCTGGCAGCGCTGGTGCACCTGCCACCCCAACTTGGCCCAACACAGCGGCCCTCTTCTGAARAC
 ATAGAGCGGGCGGTGGGCACTGGGGCCATGTTGGCTGCTCCAGCGACCTGCCCTATCTGATTGTGGGGGTGCT
 CTGGGCTCCATGTTTCTCATCTGCTGACCTTCATCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACAT
 ACACAGACCTGGGTCTTCTCTGAAAGTGCCTTCCACCTCTGCGCGTATATGTTGGTGCATTTGGAGGAGTCT
 CCAGGCCACAGGCGAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGATCCACATG
 AATAGGGGCTGCCCTCGGCTCGATGGGCTACCGGGCATGAAGCCCCAGCAGCATGCCCAAGGCGAGCTTCAG
 CAGCAGAGTGAACCCAGCAGCTGCTGAGCAGACCCATCTTGGCAATGGATATGACCCCAAGTCCACAGTACAGGAT
 ACAGGGGTGCCAGTCTAGCCCGGACGAGGGCTCTTCTTATACACTGTCGCCAGCAGCTCCACTCCACAGCT
 CTCGACGCCCTACGACGTGTCGCAACGCGCAGGAGCAGCTGCTGCTGTGGGCGGCTCAGGGGTGAGGAGAGCC
 CCGCAGCTCTGTCTGAGAGGTTGGGACCTCTCAATTTCTGCTCAGGGCCCATGCTGCTTGGGCTTGGTCTGTG
 CCAAGTTGAAGAGGTGAGACCTCTGACTCTGCAAGTGGAGTCTGCTCCCGGGGCTGCTGGTGGTCTTTTGAACACCACT
 GCTCAATTTAGGCAGAAAGCTGATATCCCAAGAAAGCTATATATGTTTCTTTTAAAAAAAAGAGAAAAA
 AGAGACAGAGAAATTTGTTATTTATTTTCTATATAGCCATTTATATATTTATGCACTGTAAATAAATGTA
 TATGTTTATTTATTTCTGGAGAGACATAAGGAGTCTTACCGTTGAGGTGGAGAGGAAATAAAGAGCTGCA
 CCTAACAGGAGTCAACCCAGAAAGCCCGCAGGGTGGCGGGGACAGACTCAACTGCTGGGCGCTCTGCACTG
 CGAGGCGAGGCTCGAGGAGGCCACACAGATAAGCTGGCAAGAGAGGATCCAGGCACATGGTTCATCAGGACA
 TGGAGGACAGCAAGGGGACAGGATATCACAGCTGGAGACACCACACAGATGGTGCATCCGTCAGTCCGGGAA
 ACATTTTCTAAGATGCCCATGGAGAACAGCAAGATGTGACAGCAGTATGAGCATTTAAAGAACTTCCAGAT
 CATAATCCGTGCAACATATCTCTAAAAACAACACTGTAACTCTAAATAGTTTAAAGCTTCCCTGTAATA

FIGURE 36

MLRGTMTAWRGM RPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGT VILGCVVEPP
 RMNVTVRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQC VARMFAGAVASVPATVTL
 ANLQDFKLDVQH VIEVDEGNTAVIACHLPESH PKAQVRYSVKQEWLEASRGNYLIMP SGNLQ
 IVNASQEDEGMYKCAAYNPVTQE VKTSGSSDRLRVRRSTAEAA RI IYPPEAQTI IIVTKGQSL
 ILECVASGIPPPRV TWAKDGSSVTGYNKTRFLLSNLLIDT SEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCM AENEVGSAAHAVVQLRTSRPSITPR LWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASP KCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFR TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRNGGFFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIYPASNNT
 PIHGFYIYRPTDS DNDSDYKKDMVEGDKYWHS ISHLQPETSYDIKMQC FNEGGESEFSNV
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRAWSKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRCGPSAAVGYPGMKPPQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSFVLEAVWDPPFHSG
 PFCCLGLVPVEEVDSPDCQVSGGDWCPQH PVGAYVGQEPGMQLSPGFLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

10005769.120601

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCGGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGTCCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTTGGACCTTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCCAAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCCTCCTACTCTGAACCTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGATTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCCCTATGCATCGGACACCTTGATAAGAAGGGTCCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTTCATCGGGATTGGTGGAAATATGACGGGACT
 GGCCGCTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCCTGGAGGTCTCCAAATGCCT
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGTGCCACCATCCCAACCTTCACCCAGTGGCTC
 TGCT**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGAAAA

FIGURE 38

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRLRRLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLNRFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVFWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

1006768-120601

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTGGGTGTTTGTGTTGCCCCAGCTGAAGCCAACAA
 GAGTTCGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCGTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**TGGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCCTCCTT
 CTCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTACCCCTTGAAGATAAAGCTGGGTCTTCA
 GGAACCTAGTGTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGTTCTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACCTGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAAGTGCATGGA
 GAGAAAATTTTGCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG
 TTTTATTTCTCTCA

FIGURE 40

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNSQKDCNCLHVVEPM
PVPGHDEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

1006768-120601

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAAATTTCTGTCCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCTCCCGA
 ACCAGGAAGGGTTGAGGAAACACAAATCTGCAAGCCCCCGGACCCAACTGAGGGGGCCCGTGTGGGGTCTTCC
 TCCCTTTTCATTCCCAACCCCTCCGGGCTTTGCGTCTTCTCTGGGGACCCCTCTCGCGGGAGTGGCGCGGTTGATG
 CGGAGCAAGGATTCGTCTGTCTGCTCTACTTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGAGCT
 TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAGGCGCCCAATCGATCTGG
 GGCATGTACCAAGGACTTGCATTTCGGCGGCAGTAAGAAGGGGCAAAACCTGGGGCAGGCTACCCCTTGTAGCAGI
 GATAAGGAGTGTAAAGTTGGGAGGTATTGCCACAGTCCCAACAGGATCATCGGCTGCATGGTGTCTCGGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTCTGCCCCAGTACCCTGCAATAATGGCATCTGTATCCCAAGT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGCAACAGAGATCGAAACCGACGGTCATTAC
 TCAAAACATGACTTGGGATGGCAGAAATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
 CCAGTGTCCATCAGGGGGAAGTCTGTACAAACACGCAAGAAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
 TGCAGCTGTGCGAAGGGCGTCTTTCGAAAAGTATGGAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAATTTTATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTATTTTAAATGCATTATAG
 CATGGTGGAAATAAGGTTCAGATGCAGAAGATGGCTAAAATAAGAAACGTGATAGAATATAGATGATCACA
 AAAGGGGAGAAAGAAACATGAACCTGAATAGATTAGAAATGGGTGACAAATGCAGTGCAGCCAGTGTTCCATTATG
 CAACCTTGTCTATGTAATAATGTACACATTTGTGGAATAAGTCTATTATTAAGGAACACAGCACAGCTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
 TTTATCAAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTTAAACAAAATCTCCPAGAATAACTTGTGA
 TACAATAGGTTCTAAAATAAAATTTGCTAAAACAGAAATGAAACATGGAGCATTTGTTAAATTACAACAGAAAT
 TACCTTTTGTATTGTAACACTACTTTCTGCTGTCAATCAAGAGCTCTGGTAGATAAGAAAAAATCAGTCAATAT
 TCCAAATAATTTGCAAAATATGGCCAGTTGTTTAGGAAGCGCTTTAGGAAGACAATAAATAACAAACAGACAG
 CCACAATACTATTTTTCAAAATTTTAGTTTACCTGTAATTAATAAGAACTGATATAAGACAAAACAGTCTCC
 TTCAGATTCTACGGAATGTACAGTATATCTCTCTTTATCCTATGTGATTCTGCTCTGAATGACATTATTTTCCA
 AACTATACCCATAAATGTGACTAGTAAATACTTACACAGAGCAGAAATTTACAGATGCGCAAAATTTTAAA
 GATAGAAITAGATTGGTAAATACATGTATTATACATACTCTGTGGTAAATAGAGACTTAAAGCTGGATCTGTACTG
 CATTAATTTTACTATGCAGATGAATCAGTGTGAGGTCCGTGTGCGTACTATCCCTCAAATTTATTATTATATAG
 GAGCACAAGTTGGCTGTTTCATCTTTGAACACAGGGGATGCACAGTCTAATATGAATATCTGCATGGGATTGTCTAT
 CATATATTTTACTATGCAGATGAATCAGTGTGAGGTCCGTGTGCGTACTATCCCTCAAATTTATTATTATATAG
 TGTCTGAGATCTCAAATAATCTCAATTTCAAGGAGTTTCACAAAATGTACTCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATGGCCCTATAAGACTCTGACTAGCCAAATGGCATCATCCAATTTTCTTCCCAAAGCTCTGCGAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCCAGTTTCTAAATTTCTTGAACCCACTTTTACTCTTTTAAAACTT
 AACTCAGTTCTAAATACCTTTGCTGGAGCACAAAACATAAAAGGTTATCTTATAGTCTGACTTTTAACTTTT
 TAGACCACAATTCACCTTTTATGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
 AGATTGAGTTTGAACCTGTATATCTATTAATAATTTCAACTTCCACATATATTTACTAAGATGATTAAAGCTTA
 CATTCTTGCACAGGTCTGCAAAAACAAAAATTTATAAATAGTCCATCCAAAGAACCAAGTTTGTATAAACAGGT
 TGCATATAAGCTTTGTAAGTGAATGAAATGGAACATTTCAATCAACATTTTCTATATAACAAATTTATATATTACAAT
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAAATTTTATTACAGGAAATG
 TTAATGAGATGATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAAATATTTTGCAGCTATGTAGC
 TTTGTAAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAATTTTCTCTCTATAAAACTGAAAAAATAA
 AAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTTRHRDRNHGHSNHDLGWQNLGRPHTKMSHIKGHEGDPCRLS
SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

10006768-120601

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCGTATTGTGAGGATTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCACCACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACGTGTTCCCTCT
 CCTGGTTTGAGTCTTTTCTTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCACCTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGCTG
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGCGGATACCCCCAGCTTCTAAG
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGCAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAACACACAGTTGGTCAATGGCTCATTTCGTTAAAGCAGCCCTTTTGGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGTTGGCGGCGCTGCCTGTAATCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

10006763.120601

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
PGLESFSPQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVDTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

1006766-120601

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**CGCTGCCATCCCGAATCCTGCT
 TTGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCCGACGGCCCCCGGCCACCCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG
 GTCCCGCACGACCGCGCGGACCGCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTCTGCGCGACCGGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACCTACTCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCACAG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTTTCATCCTGCTACTGGTCAC
 TGTCTCTGGCCGCCCGCAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGACAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCTTCCAGCGGCTGGTCCCGCTTTCTCT
 GGAATTTGGCCTGGGCGTATCGAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCCTTGTCTACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAAGTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGTCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTAAAAA
 AAAAA

1006758.120601

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLDRVAVGADAFERGFDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPRGSPGNGSSHS GAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDL DKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

10006758.120601

FIGURE 47

CGCCGGAGGCAGCGGCGCGCTGGCGCAGCGGCGACATGCGCCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
 GGACCCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG
 TGGCCCTCATGCTGTGCTGGTGGCCAACTTCTGCTGTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACCTGGTGAA
 GGTGGACACTTCCCTCTGGACCCGTGGTTTTTTTTGGCGGTACCAATGTCTGCATGGTGATCC
 TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCTGTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTGGTGGCCTCCAGATTCAATGATTCCACACACCCCTCTCC
 GCCCATCTCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC
 AGCCTCATCTACCCCGCGCTGTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCCAGCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACATTTGCTGACCTAT
 GTGGCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGCGCTCCACGGG
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTCTTCTGTGCTGTGTAACACCAGCCCCGCGT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCATAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCCTCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCACGTCCATGCCATTTCCGTGCAAGGCAGATATTCAGTCAATATTAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCT
 GACAGCGAGATGCAAGCAATGCTCAGCTCTCTTACCCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCAGTCTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGTTGAACAACCTGCCACTAACACAGACTGGAAACCCAGAAAGATGGGCCCTTCCATGAAT
 GCTTCATTCCAGAGGGGACCAAGGGCCCTCCCCTGTGCAAGGGATCAAGCATGCTTGGCCCTGGG
 TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGCTC
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
 GTATTCAAAAA

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FIGURE 48

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFVLVCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSASVSRFIDSHTPPLRPILKKTASLGF
CVTYVFFITSLLIYPVACTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

100676.120601

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCACCCAGAGT**CATG**GGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGGTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGCGCCGGCGTGACGCTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGCCGGGCTTGTGCTGTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCGCGCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTAAGCTTCCGAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTCTACCCGCCGC
 CGCGCGAGGGCGCGTCTGCTGGCCTCGTACACGTGGTCGGAGCGCGCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTGCTGCCAGCTCTGGGACGGCACCGCGTCTGTCAAGCGTTGGGCGGAGGACAGCACA
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCTTACCCGCACGGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
 GTGGCCAGCAGCCCCTCGATGACCTGGCAAAGGAAGAAGCGACCCACCCTCCAGTCCAAGG
 CCAGTTATCTCTCAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGA AAA
 AA

1006768.120601

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPFARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPFWREEHIEGG
HSNTDRPSRMIFYPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

10006758-120501

FIGURE 51

CTGACATGGCCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGCCCTCTGCTGCAT
GGACGCTCTGAAGCCACCTCTGTCTCGAGGAACACGAGCGAGGGAAGAGACAGGACCTCGTGTGGCAGGAA
 GAACCTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGGCGGCCCTCTCGAGGGCTGAATTTCT
 GCTGCTGTTTACAAAGATGCTTTTTATCTTTAACTTTTTGTCTTCCCACTCTCCGACCCCGGGCTGTATCTGCAT
 CTTGACATTTGGAGCTGGCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGCTCTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGGGAAGGGGTTTCCCAAGAAACAATGACCTAAACAATTTGCTG
 CTCTCAGATGCCAAGACTATGATGAGGTTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTTGGG
 ATATAGAAAACCAACCCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGACAGATACCTGGGTTCT
 CTGTCTCTGCATAAAAGGATATAAATCATCACCAGACCACTTTGTCCGCACTTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACAGAAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCTGAAGGTGATCATCTTATGACACCTTTGATGATGACCTGAA
 GCAAAAGAGGGGAGAAGATGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCAGGCCAAAGAGCACTTCAG
 AAAACCTGTGCTCTTAGCCCCAGAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGTATACCCATCAAAATATTTGTTCAAATGCTGCTGCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTTGAAGAGGATGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTCCCGCGGTGCCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAATAGAGGCCAAGACACCCCTT
 GAAGAAGTTCTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCTGGCGGAAGGTTGCTGTAAATTTGCTCAGTGGAGC
 TGCCCCCTTGCCACTTCACTCAACATCTTTCGGGGCACTGGATCTCAGTGTCTATCAAGCTTATGGCTCA
 AACAGAACTGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGTCACCTTGGGTTGCCCTGGC
 TTSCAATTAAGTGAAGCTGGAGACATGTGGCTGACATGAACACTTTACAGTGAATATGAAGGAGAGGTCTGCAT
 CAAGGCTACAAAGCTGTTTCAAAGGATACCTGAAGGACCTTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTCCACACAGGACATTTGGTCGTGGCTCCGGAATGGAATCTGAAGATCATGACCCGTAAAGGAACATTTT
 CAGCTGTGGCCCAAGAGATATGATGACCAGAGAAGATAGAAAATATCTACAAAGAGGTCACCAAGTGTGTACA
 AATTTTTGTACACGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC
 ATTTGCAGCCAGGCTTGGGGTGAAGGGCTCCTTTGAGGAAGCTGCCAAAACCAAGTTGAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAAATTTGGGAAGAAAGTGGCCTTAAACATTTTGAACAGGTCAAAGGCATTTTCTTCTATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAAAGCGAGGAGAGCTTTCCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGGCCACTG
 TGCATGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCCCTCTATTTTTTTTTAAACC
 TGTAAACTCTAAAGCCATAGCTTTTGTTTATATTAGACATATAATGTGTAACCTTAGTTCCCAAATTAATCA
 ATCTGTCTTTCCCATCTTCGATGTTGTGTAATATTAAGGCTTCAGGGCTACTTTATCAACATGCCTGTCTTCAA
 GATCCAGTTTATGTTCTGTGTCCTTCTCATGATTTCCAACTTAACTATTAGTAACCAAGTTCAAGGGT
 CAAAGGGACCTCTGTGCTCTTCTTTGTTTGTGATAAACATAACTTGCCACAGTCTCTATGCTTATTTTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATCTGAAAAACTGCTTACAATTCATGTTTCTAGCCACTCCAC
 AAACCACTAAAATTTTAGTTTTAGCCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAATTTGTGTACTGAAGGGAAAGTTTGATCATACCAACATTTCTCTAACTCTCTAGTATAGATA
 CTCGATCTGGGAGTATTAATAATTTGGGCTCTATGACATCTGTCCAAAGGAATGCTGTTCTTAAGCACTATTATA
 CAGTAGGAATCGGGAGTAAATCTGTTCCCTACAGTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGATGTACA
 GGTGGCCAGTGAACCTTTCCAGATAAATGAAGCAAGCACTGAATAAAAACTCTTGAACTGGGAACAAAGATCT
 ACAGGCAGCAGATGCCACACACAGGCTTATTTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGGAAT
 AGAGTTCTGTCTTACTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGCTTTTAAATAAAC
 TATTACAGATAAAAAA

10006768.120601

FIGURE 52

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
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CCFSDAKTMYEVEFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYSKSS
PDQFVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLVIIILMDPFDDDLKQERGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTDDVAISYLPPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPVAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGVRVVIIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTPLPGDWTSGHVGVPACNYVKLEDVADMNFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSLSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFISIENGLLTPTLKAKEGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

10006768.120601

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCCCTAAGCCATTCTGTAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGT**ATG**GAGCAGCTGGAAGCCACGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTCGGGAGATTCTGTCA
 GACAGGGGCGCGTGCTTTTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCCAATGAAGACCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCGCGCTTGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACACGGTGCTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGCTGTGTTTGACACGTACTACCTCATGAGGATGAGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACGTCTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCT
 TAAGTCACTGCCCTCTCTTCTGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCTCAATGTGCCTGTGGCTGTATTGCGAG
 GGAACCGACCCAAATTACTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT
 CCTCAGATGATAACAGTGTTCATTGACGGCTACTATGAGAACCCATGGATGTGTGGCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAAATGCCCGGTCTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCATACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCTCCTTGAGC
 TTTCCGATCTACCACCTTGGCATCGTCGGGCTCAACATGAATGGCTACTTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAAGAGCTTATGAAGTGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCTCCA
 TATCTGGGACCTGGATGTCGCTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGGTGGTGGGGTCCGGCTTCCCCCTACTCAGTGAAGAAGGCCACCCCTCAGTC
 ACCCAATTTTCTGGAGCCACCCCAAGAGGAGGGAGCCCCAGGAGCCCCAGAGAACAGAC
ATGCACCTCTCTCAGGACCTCGCGGGCTGGGTACTGTGTACCCCAAGCTGGCTAGCCCT
 TCCCTCCATCCGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTAAACA
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT
 AAAAGTCTATTATTACTTCTTCTTGTGGAGAAGGCCAGGAGAGTACCTGGGAATCATTACG
 ATCCTTAGCAGCTACTCTGCCCTTTGAATACCTCACTTCCAGGCTGGCTCAGAATCTA
 ACCTATTATTGACTGTCCTGAGGGCTTGAAACAGGCCGAAGCTGGAGGGCCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACCTGCTGTGCC
 CAACCCATTGGACAGGCCAGCTGGGGCCACATGCTGACACGACTCACTCAGAGACCCCTTA
 GACACTGGACCAAGCCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCAAAGCTGGATAAGTT
 GGTCAATTGATTA AAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

```
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REQGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSGAGPALGWRDTHAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTPVPGVQLRNVDLSLKKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDEFTTWTQLAKCLHIWDLVDRGNHRGLWRLFRKKNH
FLVVGVPASPSYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

1006763.120601

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACTAAGCACCATTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAA**ATGG**ATGATTTTCATCTCCATTAGCCTGCTGCTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGCTGTTAATTTCTCAGAGGAACCACTGAAGCTGGTACTGTTTGTGG
 GTGCTGGCCTTCTCTGTGAAC**TGCTCTGGCAGT**CATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTGAGGGAAAACACCAAGCAAGTGAACACATAAATGTGATTGCAATGCAGACAAAGCAG
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCAGCACCACACAGCTGCATGCCATATATTTGGTG
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 ACTGACGATCCAGAAGCAGCAAGGCTAGCAATTCCAAATCACCACCAGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCAAGACCAAGTGTCCAGTTAATTTG
 TGTGTTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCCTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCAT
 GGTGACATACTTAGGACTGAGTAAGACAGTAAAGAAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
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 ATAGGGCAGACGCCACAAGCCGATGCCACGGGAGGGAGAGGCTCAGCCGCTGGAAAGTGGCAGCCCT
 GGTTCCTGGGTTGGCTCATCCCTCTCATCTGTCAAGTAGGACACCAGCAT**TAA**ATGTTCTCAAGGTCCAGC
 CTTGGTCCAGGCGCGTTTGCATCCAGTGAGAACAGCCGGCAGCTGACAGCTACTCATTCTCTCAGTC
 TCTTGTCTCACCTTGCGCATCTCTACATGTATTCCTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTTG
 AGTAATGGAAAGCTTTTAGAGTAGAAAACACATTACGTTGCAGTTAGCTATAGACATCCCAATTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTAACCTATTTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGA**ACTT**CATACTACAATGAAATAGTGATTATGAAATACAGT
 GTTCTGTAATTAAGCTATGCTCTTCTCTTAGTTAGAGGCTCTGCTCATCTTATCCATTGATTTTT
 AACATGGTTCACCACATGTAAGACTGGTGCTTTAGCATATATGCCACATCGGTTGATGGAAGGTCATA
 GCACCACTCATTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGTCAGGAAATGATAGC
 AAGACACATTGAAGCTCTCTTTATATCTCAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTGTCAAGTTCTCCTTGCAGAAAT
 ACCGTGCTCCACATTCCTAGAGAGGAGCCAA**GTTC**TAGTAGTTTCAGTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCACAAAGTGCTTTTGGAAATTAAGGGATATTAATTTAAGTGATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTAAAGACTACCAAATGATGGTTGCTCTTTTTTTTTTGT
 TTTTTTTTTAATTTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTACGCTTT
 GCGGACACTGTGCTTCTCATAAACCACTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA
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 TCCCTCTAGCCTCTCTCGGCCACAATTTGCTGCTTACTGCTGGTGTAAATTTTGTGTGGGATGAAT
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 ATTTTTTTTTCATATTTGCCAAAATTTTGTAAACCGTGTCTTGTCAAATAAGTGATATAATATTGTAT
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 GACTGGTGTGAGACTTGAGTTTCATCTAGTCCTCAAACATATAGGTTGCCTAGATTCTCTCGGA
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGCAAAAAAA

10006768.120601

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

1006758.120604

FIGURE 57

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCGATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACCCAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
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 AATCATACACTCTGAATTGAATGGAATCACATATTTCAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

1006768.120661

FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTAPSSSEVVLDSKR
QVEKEETNEIQVVNNEEPQRDRLPQEPGREQVVEDRPGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

1006768-120601

FIGURE 59

GGATG CAGAAAAGCCTCAGTGTGTCTCTCTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTTGCCCTCTTCA
 CCAGTGGCTTCTCTGCTCACCCGTTTGGAGCTCACCACCATAGCAGTGCCTCAAGAGCCCGCCAGGCGCTGGGTCCC
 TGCCATGGGGGAGCCAAAGGGAACCTGGGCGCTGCTGGATGGCTTCCCGATTCTTCGCGGGTGTGTGTGGTGTCTGA
 TAGATGCTCTGCGATTGTGACTTTCGCCAGCCGCCAGCATTCACACGTGCTTAGAGAGCCTCTGTCTCCCTACCCCT
 TCCTGGGCAAACTAAGCTCCTTGGCAGAGGATCCTGGAGATTACGCCACCATGCCCGGCTCTACCGATCTCAGG
 TTGACCCCTCTTACCACCACCATCGAGCGCTCAAGGCCCTCACCACTGGCTCTACTGCTTCTTATTTGATGCTG
 GTAGTAACCTTGCGCCAGCCACGCCATAGTGGAAAGACAATCTATTAAAGCAGCTCACCATGCCAGTGGAGGAGCGGTAG
 TCTTCTATGGGAGATGATACCTGGAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCTTCA
 ATGT CAGAGACCTAGACACAGTGACAAATGGCATCCTGGAAACCTCTTACCACCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTCTGGGTGTGGACCATCTGGCCACAGCATGGCCCTCACCACTGAAATGGCCA
 AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGCTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGCCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTCT
 TGTATAGCCCCACAGCAGTCTTCCCGACACCCACCAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTTGTGC
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 TTGCTGAGCTGCAGCACTTCTCTCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGGCTCGTCTTCTCTGGTCC
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 TCTGGGAACCTATTGAGCTGAGATAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTCACTCTCCCTCTT
 TCTGTGGAAAGCTCGGGCTGGCTGGGGGTCCAAGAGGCCCTTGGCAACCTCTTTTCCATCCTCTGGGCGCTGCC
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 TCTCTTTGGGCTCATTTCACTCTGCTCTGCTGGTTGTCCAGCTTCACTGGGAGGCGCAGCTGCTTCCACCTAAGCTAC
 TCACAATGCCCGCTTGGCATCTCAGCCCAACAACACCCCGCCAGGACAAATGGTGATATGCCCTCAGGCTGTG
 GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATGCTTGGCCCTGAAGAGACACTGTTTGGCAT
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 TCTACCGACATCGAGGAGGAGTTCGGGGGCGGTAGAGAGGACCAAACTCAGAGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGGAGTGTTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGCTTCCCATCTTCTGCTGT
 TGCATCGGAGCGCATCAGCCTTGTGTCTGCTTCTGTTCTGTCAGAGCTTCTCTCTCTACATCTGCTTGGCTG
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 CACAGACCTTCTACTCCACAGGCCACCAAGCTGTCTTTCAGGCATCCATTGGCATGCAAGCTTCTGGGATCC
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 TTGCACTAGGTTCGCCACTGCTCTGCTCTGGCTTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
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 TGGCGTGTGCTTGGCAGCTCTTCTCGCAGGCATCTCAGTGTCTGGAAGTGTCTGGCCCTAAGTTCATAT
 TTAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGT
 CTGTGAGCTCTGGTTTCAGGCAGCTATTCTTGGCCAGCAGAGGTAGCTAGTCTGATTTAGTCTGGCACTTGGCT
 ACAGAGATGCTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGACAGCAGGCTCAGCCATAC
 TCTTACTATGCTCAGCCAGGGGCGCTGACATCTAGGACTCTATTATTTCTATTAATTCAGGACACAGTGGAGTA
 TGAATCCCTAATCTGATTTTGGATGCATCTGAGGACACAGGGGGCGGTCTCCGAGTGGAAATAAATAGGCCGG
 CGGTGTGACTTGCACCTAATAATCCAGCACTTTGGGAGGCACAGCTGGGAGGATGTCTGGTCCGAGAGTTCA
 AGACCAGCTGTGGAACATAACAAGACCCGCTCTCTACTATTTAAAAAAAAGTGAATAAATGATAATAT

1006768.120601

FIGURE 60

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVIDALRFDFAPQHQSHVPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGTSLPTFFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPSEFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISSPGFPFCPLLLTPVAWGLVGATA
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLLA
VFFSDSFVVAEARATPFLLLGSFILLVQVQHWEGQLLPKLLTMPRLGTSATNPNPRHNGAY
ALRLGIGLLCLTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRLVSVGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLFLQSFLL
LLHLLAAGIPVTPPGPFTVPWQAVSAWALMATQTFTYSTGHQPVFFAIHWHAAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFVAGCPLLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFIQILACALAAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

1006768-120601

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**AATGT**
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTGT
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTC AAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTCTTCTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA
 GATTCTTTGTGCTGCTGAAAAAATCGTGATTAACTTTATCACCCCTCAATATCTCGGATGAT
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAGAAAAACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAAACAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGACGGCAGCGTTGGCAGTCTTGGGCCCCG
 CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCCTGGTCGACTGGGATCCCC
 AAACCTGGCAGGCTGTGTATTCTTCGTGTECAGCTTCGACCAGGATTAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGAAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTTCTGTGCAAAC
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTCATGCAGAAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTACGG
 TGGGTGT

1006768-120601

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGEKEHPANLILYGNFED
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYDYVTRTTDICAGPEEQELSL
QEEVSTQGTLLSQAAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

1006763-12601

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCCTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGCGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCGAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCAGCCCCGGCCCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCCTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTACAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAAAAAAAAAAAAAGAAA

1006768.120601

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPFYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPVGLLRLLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLTMLCTRSGDSHRRGFC SADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

10006758-120604
100021-8975001

FIGURE 65

GAGCTACCCAGGCGGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCCGGCA**ATG**AGCCGCTACCTGCTGCCGCTGTCCGGCGTGGGCACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGAAAGATCATTGAAGAGGAGGACGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCGAGTTTGGCGTTAACCACCTGGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAGTACTTTCGATGGACTCAAACAGAAAGCCCCGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCCGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCCAGAT**TAA**CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGGCCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACCTTGACAGCCACGTGAGGAGACCCAGCGGTGCCGTGCGGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCGATGGTCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGCTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCC
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TGTCCCTGGGACTCCCACCTTCCCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC
 TTGCTCATTT

1006768.120601

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

10006768.120601

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCCCTGGCGCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGCTGCGGGACCTGACTAGATTCTACGACAAGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCTGATCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCACTCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAAGCCCTGGGTTCCAGGCCACTCTCTACCAGATCCCTAGCCTCTACTGTTTCCTAT
 GAGACCAATTTCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCTCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGCTGGCAGGAGGAGGAGGAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA
 CCACCGCATTTGCTGCCCTCAGGCGCTTGATGTCGGGCGCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAAGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGCTGGTGGGAGATAAGTGGGTGGCCAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCTGTCAGCTCCAGCCCTGAAGACT**GTA**CTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCCTCGCAAAATCAGAGGC
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTCCGATCAGTGGGTG
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGAGGAG
 GGGCTAGCCTGACTCCAGAACTTAAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTT
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTAACACAGTCATTAAAA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLYKERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

10006768.126601

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTGGGAT
 CTGCCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGGAACCAGACCATTG
 ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTTGAGCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC
 AAGGAGCGTTTTAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCGGTGATCAT
 CTGGTTCATGGACAACATACCCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCGCTGTGTGTAGGTCCACGGCCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACAGTTTGTAA
 TCAAACAATAAAAAATGTTTTTGTGTTTTTAAAAA

1006768.120601

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLIISTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILLGVVMFMVSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALFRNQTIIDFL
NDNIRRGIEYNYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIWFMNDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

100676-12661

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGCGCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCACTGCACTTCTCATCCTCGGCCCCAAAAGTCATCAAAGA
 AAAGTGCACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAAGCCACCATC
 CGCATGGACACCAGTGAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTGAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTTCATGGTCTGTTGG
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCACTGATCGTGTGGAAGTGTTCCTCTCCA
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGGTGCATTGGTG
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMTPTLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTkdALVLTpasLWKFPSSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

1000676.100001

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGCTCGCCTTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATCCAGATCCTGGC
 AAACCTCGCGGATACCTCCAGTGCATTACCAACAGGATATTTTTGGCCATGGTGGATTTTG
 ATGAGGCTCTGATGTATTCAGATGCTAAACATGAATTCACTCCAACCTTTATCAACTTT
 CCTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTTATGCTGGTCCCTTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGACGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTGATTATTTCTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAGGTTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAATCGTGTGTGTTGAAAAGAAGATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACTTCTCTT
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTTAAAAAATTGAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCACTGTAT
 TTTATATTGCCTTATCCAAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTGATGTTGCTTCTGAAAATG
 GAACACCATTCTCAGAGCACACGCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA
 GATTTCAAGATTCAATCCATCTCCTTAGTTTTCTTTTAAAGGTGACCATCTGTGATAAAAAAT
 TAGCTTAGTGCTAAAACTCAGTGTAACCTTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGCGCACTGACTTACGCTGTAATCTCAGACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCTTGGCCACACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAACTCACTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCATCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

1006768.120601

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWNTNKRVPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

1005768-120601

FIGURE 75

AAGCAACCAAACGCAAGCTTTGGGAGTTGTTTCGCTGTCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCGGCTGGCCCCGGCGGCAGGCTCTCAGAACCGCTACCGGCGCATGCTA
 CTGCTGTGGGTGTCGGTGGTTCGACAGCCTTGGCGCTGGCGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTGTGGTGGAGGCATCCTTCGATG
 GAAGGTTAAACATTTCAATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG
 ACAGTGGGACTTCCTTTCTGAATGCCTACACAAACTCTCCAATTTGTTGCCCATCACGCGC
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAAGGCTCTAG
 ATCCAATTTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAGGCGAGGCCATGGTTAATCTTATCCGTAACAGGA
 CTAAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTAACACTGAACCATTTGTTATTACTTGGGATTAAATTTACACACCC
 TTACCTCTCACCATCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
 GGCTTGAAAAAGTGTCATGATGCCATCAAAATCCCAAAGTGGTCACTTTGTGAGAAATG
 CACCTGTAGATTATTACTCTTCTTATACAAAAACATGCACTGGAAGATTACAAAAAAGA
 AATTAAGAAATATTAGACATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AAATTTATTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACTCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGTATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAATG
 TGGTTTCTCTTGTGGATATTTACCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATACTCTTTGTTGCCGTATCATCAGAAACATTTAAGAATGAACATAAAGT
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTCCGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAATTTCC
 AGAATTAATCTTATCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCATAAGTTTCTG
 CTTCTGTCCACAGTATAATAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT
 TATTCAAAGCTTATAGCAAATCTTAGGTGGCACCAGACTGGCGAGGAACCAAGGAAGTA
 TGAATGCAATTTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA
 GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGATTTT
 AAATGAAACAGTTTAAATAATTACCAAGTTTGGCCGGGCAAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC
 CAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATAGCTGGGCGCGGTGGTGACA
 CCTATAGTCTCAGCTACTCAGGAGTGGGAGGAGGATCGCTTGAAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGGCCACTGTACTCCAGCTGGCAACAGAGTGAGACTGTGTGCG
 AAAAAATAAAAATAAAATAATAAATTTTCAATTTTGTAGAAATGATGATG
 TATTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAATGGTTATTATTTA
 GGCCTTTGTACAAATTTCAACAAATTTAGTGGAAAGTATCAAAGGATTGAAGCAAACTACTGTA
 ACAGTTATGTTCCCTTTAAATATAGAGAATATAAAATATGTAATAATATGATATCAATAAAT
 AGTTGTATGTGAGCATTGTATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

1006768.120601

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRITFHPGSQVVKLPFFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSFTHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPIKAGLQVSNVSVLVDIYPTMLDIAGIPL
PQNLSGSYLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

10006753.120601

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTG**TGA**AAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCAACCTCAACTTGAAACCCCAATCCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

10006758.120504

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRICTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAWNHLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

10005768-120601

FIGURE 79

GCACCTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTCAAGGTGTGAATCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCT**TGA**GAGAAGACATAGAAAGAAAAATCAACTTTCCTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCACTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

1006768.120601

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPNLCQPAAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLVQGVNSQCHSSPISSKCESRRRF

Signal peptide:

amino acids 1-25

10006766.120601

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
 TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGCCCCCATGACTCCTTACCT
 GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
 GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
 GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
 CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAG**TAA**TGGAACATCAGGGGAA
 CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
 TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
 CTGTGACCTGTCTGAGGCCACCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
 AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
 GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCTTCACCTT
 TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
 TAAATTTATGTACTTTATAAATGAAAA

1006758.120604

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

Signal peptide:

amino acids 1-24

10006768-120601

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCGCTCCCGCCCGCTCCCCGGCACCAGAAGTTCCCTCT
 GCGCGTCCGACGGCGCA**CATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGCGAGAACGTACCCCTACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGCCCATCCGCAACCTCAGTTCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGCT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTAAACATCAGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACGCGCGTCCCGAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACC
 CCGGCTTTGAAGCCTACCACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCCAGCAC
 CCCCTGTCTCTCCAGGCCCGGAGACGTCTTCTCCCATCCCTGGACCCCTGTCCCTGACT
 CTCCAAACCTTTGAGGTCATC**TAG**CCAGCTGGGGACAGTGGGCTGTTGTGCTGGGTCTGG
 GGCAGGTGCATTTAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCCAGCCCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCCTCAGAACGTCACGCCCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGCTGGCCGCCTTGCTCCCCGCTTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCTTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCACTGGAGATGGTGTCTGAGGAGGTGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGGAAAAA

1006768.120604

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVVK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLTLDGSLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

10006768-120601

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCC
 TTTCTGCCCCACGCTGCTTCTTGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
 CTCGCTCCCGGACCAGCGGCTGACCTTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCT
 TCCTCCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCAGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCTACT
 TGGAGCCACAAGGCCTGATGTA CTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACCGCCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCACTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTTGCAGTCCCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA
 GCAGACCTTGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCAGACCTTGGAGCTGAAGGTACAGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

1006768.120601

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPDPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

10006753.126504

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATG**GATTCTTGCGGAAAATGCTGATCTCAGT
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
 AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
 CGTGCCCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGCGGCGCCAGCGGGAGGTCACCGT**T**
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGCGCTTGGGCGCAGGAATCCGAGGCAGCC
 TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
 TCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCAAACCCTGGACTGACTGCTTTAAGGT
 CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAACTGAAAGAACCAATAAAA
 TCATGTTCCCTCCAA
 AAAAAAAAAA

10006768.120601

88/249

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

10006768.120601

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCGCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTCTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCCAGCACC
 CCTCTCCTCATCTTGTTCCTTTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAGGAATGAGAAGTAC
 GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT
 GCCATGGCTGCCCGGAAAGCTTCCGAGTCCGGGTGCCCTTCCCTGGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTTCTTTATTTTGTCTCGGAGGCCCTCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTTCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA
 TGTCACAGAGAGAATGCTGAGGCTGCCTTTGTCTCTGTGGGACCCCTCTATGTCGTCTATAA
 CACCCGTCCTGCCAGTCGGGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC
 CTGAACGGGCAGCACTCCCTTATTTTCCCGCAGATATGGTGGCCATGCCAGCCTCCGCTAT
 AACCCCGAGAACGCCAGCTCTATGCCCTGGGATGATGGCTACCAGATTGCTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGAGGAGGTT**TCAG**GAGCTAGCCTTGTTTTTGCATCTTCTCACTC
 CCATACATTTATATTATATCCCACTAAATTTCTTGTTCTCTATTCTTCAAATGTGGGCCAG
 TTGTGGCTCAAATCCTCTATATTTTTAGCCAATGGCAATCAAATTTCTTCAGCTCCTTTGTT
 TCATACGGAATCCAGATCCTGAGTAATCCTTTTAGAGCCGAAGAGTCAAACCCCTCAATG
 TTCCTCCTGCTCTCCTGCCCCATGTCAACAAATTTAGGCTAAGGATGCCCCAGACCCAGG
 GCTCTAACCTTGTATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTTCTTCCCCTCAGAGTG
 ACTTGGGGAGGAGAAATAGGAGGAGACGCTCCAGCTCTGTCTCTCTTCTCACTCCTCCCT
 TCAGTGTCCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCAATTAA
 AGGAAAATCCACAAAAA
 AAAAAAAAAAAAAAAAAA

1006768-120601

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSWGPLQGQHHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGTYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWPVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAGEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ
QWDTPCPRENAEAAFFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

10036763-120601

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCTCTTCTCTCTAATCCAT
 CCGTCACCTCTCTGTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCTGTTCCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAAGAGGCCA
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTGTCAGTCCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGCTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCAGTGGAATAATCCAGGCGAACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTCTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCTCTACAGGCAACCACGCCTTCTCTCCCAGGG
 GTGAAATG**TAGGAT**GAATCACATCCACATTCTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGAGTGGCCTGTCC
 ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATCCCATCTCACAGGCTGTGGTGATAGTTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGATCTTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSIVLSLLKLGSQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFRRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLE
FGIVGLKIFFSKFQWKIQAELDWRKKGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTFFLE
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

1006763.120601

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA
 ACGAGGAGAAATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
 CCGTCGCCCTCAGCCGCTCGGCGGGGAATGTACCCGTTGGCGGGCGGGGCCGCGGGGCAAGTG
 GACGCGTTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC
 TCCCACGGCCCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCCATGTCGCCGAGACCAACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC
 ACCACCTTTTCAGGCGCCGCTCGGCCCTCGCCGACCAACCCCTCCGGCGGCGGAACGCACCTTC
 GACCACCTCTCAGGCGCCGACAGACCCGCGCCGACCAACCTTTTCGACGACCACTGGCCCCG
 CGCCAGCACCCCTGTAGCGACCAACCGTACC GCGGCCACGACTCCCGGACCCCGACCCCG
 GATCTCCCGAGCAGCAACAGCAGCGTCTCTCCCAACCTGCCACCGAGGCCCTCTC
 TTCGCTCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGCGAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACCTGTGAAACC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGACCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACCTGAAGTTTATT
 TTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATCTCTTACTTTTATATGT
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTCTCTCAAAGCACTAG
 AGTCGCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGAAAAAATTTATTGAAGAA
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGGTACCCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGCAAAAAG
 TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTGAGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTGTCCTGTACTGCACTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTGTGGACCCCAAGTCAAAAAC**T**GAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGTTTACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTTGGCAAGTAATTTCTTTCACTGAGCTTGTTCCTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCAGCGCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAAACAAATGACTGGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT
 GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGCTTAAAAAAAAAAAAAAAAAAAAAAAAA

1006768.120601

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSIPLSLGGLALLCCAAAAAASAASAGNVTGGGGAAGQVDASPGPGLRGEPSPHPFRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPPLWATAGPSSTTFQAPLGPSPTPPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDLPSSSNSSVLPTPPATEAPS
SPPEYVNCNSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

1006768.120601

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGCGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCAACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCC
ACAGCA

1006768-12694

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRITLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

10006768.120601

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGTGATTACCTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTCTGATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCCTGGAGTCCGGCTGCCCCAGAACTCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTCACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAACGCTGTCAGGGGTTACGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGAT**GGA**AAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

1006768-120601

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHL LGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWN YKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTC SVPWACEQGT PPMISWIGTSVS
PLDPSTTRSSVLT LIPQPQDHGTS LTCQVT FPGASVTNKT VHLNVSYP PQLTMTVFQGDG
TVSTVLGNGSSL SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGD TGIEDANAVRG SASQGPLETEPWAEDSPPDQPPPASARSSVGE GELQYA
SLSFQMVKFWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

1006768-120601

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AGACCCCTGTTCTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGAGGACAGGAGGCCAGGA
AGGTGTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAGACCAGCACCATGGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTACGCCCTTCAGACGGGAAGCTGCGTTCCCGAACACT**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

1006768-12691

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

10006768.120501

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GCGGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTGAGCACCA
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT
 AAGAAACCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
 GAAATATGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGATATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQFWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIIEHQKCNAYPGNITDTM
VCASVQEGGKDCSCQDGS GGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

10066768.120601

FIGURE 103

GAGCAGTGTCTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
 TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACC GAAGAA
 GTGAAAAATAGAAGTTTTGCATCGTCCAGAAAAC TGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
 AGATTGAAC TTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTAAAG
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
 GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAAGTCAC TTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
 TCTCCCAATACATTGATTTTGGTATAATAATGTGAGGCTGTTTGCAAACTTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1006768.12691

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRVVIPPSPFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFISPKYENVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

1006763-12604

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

1006763-120601

FIGURE 106

MQGPILLPLGLCFLLSLFGAVTQKTKTSCAKCPFNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

10006768-120601

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCAGACGCGCTTCTCTGTGACCCATCCC GGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCCACCGAAGCCATTCGCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTTGCGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTTCTTGGAACCT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

100676.12601

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQFWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVFGQDACQGDGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

10006758.120001

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGGAGTTTCTGTGTACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGCGAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCC
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGAGTAGGGACAAGG
 CTGCAAGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCAACC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
 CATCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTTGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTCTCTCTGCCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCGTG
 GGGTTTGGGGGAAAGGTCAGCTCAGTGCTGTTCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAAATGAGGAGTAAATGCTCACGGCAAAGTCAGAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLVM
MFEGKANESSPKFVGPPPERDIASLP

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FIGURE 111A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGGCCCTGCACACATGCCCCCGGGTGGGCAGGGGTGGCGCCCGCGCTGCGCGCC
CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGGCTTCCAGCCGTGCGCTGCC
CACCAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTC
CTCGGGGATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATATATACACAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTGGGAAGCAACAGGT
CAGCGTCTATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA
AGAATAAGCTGCAAGTCTTCCAGAAATGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAACACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT
GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACTTGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAGAAGGAGTACGTG
TGCCCGAGCCCCCACTCGGAGCGCCCATCCTGCAATGCCAACTCCATCTCTGCGCCTTCCGC
CTGCAGCTGCAGCAATAACATCTGGACTGTGCGAGGAAGGGCTTGATGGAGATTCTTGCCA
ACTTGCCGGAGGGCATCTGCGAAATACGCTTAGAACAGAACTCCATCAAAGGCATCCCTGCA
GGAGCCTTCCACCGATACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCCGA
TATTGCTCCAGATGCTTCCAGGGCCTGAAATCACTACATCAGTGTGCTGTGGGAACA
AGATCACCAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAGATCAACTGCTTGGGGTGAACACGTTTCAGGACCTGCAGAACCTTCAACT
GCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTGCGATT
CCATCCAGACACTCCACTTAGCCCAAAACCAATTTGTGTGCGACTGCCACTTGAAGTGGGTG
GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTGCAGCGAGTGTTCATGGACCTCGTGTGCCCGAGAAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACTCCC
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGAAGGGAACCACT
GGAGACCTGTCAGCGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGTGAGGA
GTAACCTGATCAGCTGTGTAGTAATGACACCTTTGCCGCTGAGTTCGGTGAGACTGCTG
TCCCTCTATGACAATCGGACTCACCACCATCACCCCTGGGGCCTTACCACGCTTGCTCCTCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGGCGGATCGTCACTGGGAACCTTAGGTGAGGACCACTTTTCCCTC
AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCGCCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTCCGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCGAGGGCATGCCAAGGATGTGACCCAGCTGTAC
CTGGAAGAGAAACCACTTAAGCCGCTGCCAGAGAGCTGTCCGCTCCGACACCTTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCTTCAAC
GGGCTGCGGTCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGCTTCTGAAGG
CTCTCTTCAACGACCTCACATCTCTTCCATCTGGCGCTGGGAACCAACCACTCCACTGTG
ACTGCAGTCTTCCGTTGGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGAGCCTGGCATGCC
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGCCAGTGACATCAACATTTGGCCAAATGC AATGCTGCCCTCCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTTCCCC

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FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGTGTCTCTGCCCTC
 TGGGCTTTGAGGGCAGCGGTGTGAGATCAACCAGATGACTGTGAGGACAACGACTGCGAA
 AACATGCCACCTGCGTGGACGGGATCAACAACACGTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCTGTGAGCTGAACCTCTGTGACGATG
 AGGCCAAGTGCAATCCCCCTGGACAAAGGATTGAGTGCAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTCTGTG
 AACACCCCCCACCCTATGGTCTACTGACAGCCAGCCATGCGACCCAGTACGAGTGCCAGAAC
 GGGGCCCAGTGCAATCGTGGTGACGAGGAGCCACCTGCCCTGCCACCAGGCTTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG
 CCTCCGCCAAGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACCTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGGCCAGGGCACGG
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCACACAGTCCCTGGGGGTGTCAACAGGTGCAAGTCTGCACCGT
 GTGCAAGCACGGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCACTCTGCGACAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGGAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGTCTAGCCTTCAAGTGTCAACATG
 GTGGGCCCCAGTGCTGCCAGCCCCCGCAGCAAGCGGGCGGAAATACGTCCTTCCAGTGACG
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGGGTGCCTCGCGTGTTC
CTAAGCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGACATGAAGGAAATGAAGCTGGAGAGGAAGTAAAGAAGA
 AGAGAATATTAAGTATATTGTAAATAAACAATAAATAAGAACTTAAAAAAAAAAAAAAAAA
 AAAAA

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FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRLVTSFNHMPKIRTLRLHSNHLCDCHLAWLSDWLRQRRTVGQFTLCMAFVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK
 GLFDGLVSLQLLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIISKGLFAPLQSIQTLHL
 AQNPFFVCDCHLKLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLEPYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRRR
 IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLNNISIMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLTLLHGNDISSVPEGSFNDLTLSLHLLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTPTTHRFQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPENLQCHEAKCIPL
 DKGFSCCEVPGYSGKLCTDNDDCAHKCRHGAQCVDITINGYTCTCFQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDLSLSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

1006768.120601

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
 CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAAC**TGG**CAAAAATATTCTCGAGGGCTGGCCTG
 GACAATTACTGGGGCTTCAGCCTTGGA**AACTGG**ATCTGCATGGCATATTATGAGAGCGGCTA
 CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
 ACAGCTTCGCGTGGTGACAGCGGAAAGCTGAAGGAGAAACAACCACTGCCATGTCGCCTGC
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
 GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
 AGTGGA**AAAAAGGCTGTGAGGTTCC****TAA**ACTGGA**ACTGG**ACCCAGGATGCTTTGCAGCAAC
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
 TTCCTTCTCAA**ACTTG**GAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTCCAT
 TTAATGTC

1006768.120601

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

10066768-120601

FIGURE 115

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCATTAAAACTTGACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCACTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACCTCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGTC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCATTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCACTCATGTCTGTTAATTCGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTTATCCGTGAACCTTCCTTAAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT
 CCACCGAAGTGTTCACTGTCTCTGTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAA

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FIGURE 116

MPLLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMOCNV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

1006768-120601

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTGGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCCG
 CTTCAGAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTCTAGATGGGTCCAC
 TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTGCAACTGCCA
 AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT
 CCTAGAGAGACCTCGTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCT
 CACTTGGATTCTCAGGCACACAGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAGAGAT
 AT**TAA**AATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTGTGAC
 TTAA

10006768.120604

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS�GTVDVLKQHINPNKTSDPFETMLKSLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQVMVGSTFE
DDQEVIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNI IKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCEVTAKLTPVSAQLQDIEGKIDRFIIPRETIVLYALGVVL
QDPNTWPSPHKFDPD RFDELMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

1006768.120601

FIGURE 119

CTAGATTTGTCGGCTTGC GGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCTTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCAACCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTGTCT
TCTGCAGTGCCCTTCAGCTGTCACTGAAATGGCTTTATTCGTACCCGTCTTTGGGCTGAAA
AAGAAACCCTTC**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCTTGGGAAGAAGGACATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAA

1006768-120604

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

1006768-100691

FIGURE 121

TCCCGGACCCCTGCCGCCCTGCCACTATGTCCC GCCGCTCTATGCTGCTTGCCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

1006768-120601

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

1006758.120001

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCCGGGCGAGGCCACAGAGGCCAGGCCAGGGCTGGAAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGGAAGGGTTGGGCCCTCAGGCAGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCTTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACAGCCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGGCCGGCCGAGA
 GCATGTGTCTGGATCTGTTCTGTGTGTCTGTCTGTGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

10006768.120601

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSPLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVLQKVCPTYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

1006569.120601

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACCAGACTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTTGGGCGGAGGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCAGCGGGCGAGACCACGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGGCTCCGGGCGCCGGGCGCTGTCCCGGTTGCCG
 GCCGTGCTGCTGGTCCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGAECTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTACAGTTTCAGTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCCTTTCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTCACAGATTATTTGTG
 TGTGCTGTTTTAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATCTGAATTCATTCTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTTATTCCCTTGGAATTAGTTTGTGTTGGTTCTTGTA
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAA
 GAATGCTTCATAGTTGATTTTTAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACCTTTATTGC
 TCAACTTTAATTAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGCTTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

1006768.120601

FIGURE 126

MSGRRALS AVPAVLLVLTLPGLPVWAQNDEPIVLE GKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFS AVRSTNHEPSEMSNKTRI IYFDQILVNVGNFFTLESV FVAPRKG IYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAA TNGVLLYLDKEDKVYLKLEGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

1006768-12601

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTTTACAACCAGCGCTCCAGATTAACCCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCTTTTTCTGAAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

10005768.120501

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSYYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLPGTVGIHGDSPPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

1006768.120601

FIGURE 129

CGGCAACAGCCGCGCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTCGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCTCTCGGTGAGAGGCCATCTGGGGGTTCTGGGGCCCCAAGACGCTCTCGCAGAAAGACGCCG
 AGTTTGAGGCGACCTACGTTGGAGCGAGGTCAACAGCGAGTGGTCAACATCTACACCTCTCAACCATCTGTGACCC
 GCACAGGACAGAGGGCGTGGGTGTCTGTGAACGCTCTGAACAAGCAGAGGGGGCGCCCTGTCTGTTTGTGG
 TCCGCAAGAGGGCGTGTGTCTCTCCAGGTGCCCTTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAACGAACCTGTCTCAGCCCCACCAAGAATGAGTCGGAGATTCACTTCTCTACGTGGGATG
 TGTCCACCTGTCAACAGTCAACACCATACCCAGCTCCGGGTGAGCGCATGGACGATTTTGTCCTCAGGACTG
 GGGAGCAGTTCAGCTTCAATACCAACAGCAGCAGACGCCCGAGTACTTCAAGTATGAGTTCCTGAGGCGGTGGAAT
 CGTAAATTGTCAAGTGAACCTCCAACAGGCGCTTCCCTGCTCAGTCTTCCATTCAAGATGTGCTGTCTGCTCTG
 TCTATGACCTGGACAACACGTAGCCTTCATCGGCATGTACAGACGATGACCAAGAAGCGGCCATCAGCCGTAC
 AGCGCAAGAGCTTCCCCAGCAACAGCTTTATGTGGTGTGTGGTGAAGACCGAAGACCAGCCTCGGSGGGCT
 CCCGTGCTTTTACCCCTTCGCAGAAGATGACCGGTGATCAAGGGCACCGCCAGAAAAACCTGTGAGTGTGG
 TGTCTCAAGCAGTACGCTGTGAGGCATACGTGAGTGGGATGCTCTTTGGCTGGGTATATTTCTCTCCTTTTACC
 TGTGACCGTCTCTGCTGCTGCTGGGAACTGGAGGAGAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
 CCTGCCCAAGAGCGGTACCCCTCGAGTCTGGCTGATTCTTTCTGCGAGTTCCCTTATGAGGGTTACAAT
 ATGGCTCCTTTGAGAAATTTCTGGATCTACGATGGTGTGGTGTGACAGCGCTGGCATGGGACCTCTCTTACG
 GTTACCAAGGGCGCTCTTTGAACCTGTAGGTACTCGGCCCGGAGTGGACATCATGAGCTCTGTGGAGAGGATG
 ACTACGACACATTTGACCGCATGATTCCGCAAGAATGTCACTCGCAACAGCAATACCTCTATGTGSGCTGACC
 TCGGGCAGGAGGCAAGGGCTGTTCTGGGAAAAAGTACCAAGTCACTTCTGTGAACATTGCCACCTTGGCTGCT
 TCTATGCCCTTCTGTGGTGCAGCTGTGTATCAGCTACCAAGCGGTGGTGAATGTACAGCGGATCAGCAATCT
 GTACTACAACTTCTCTCGCCCTCCCAACCCACTGGCGCAATCTCAGCGCTTCAACAACATCTTCAGCAACCTGGGGT
 ACATCTCTGCTGGGGCTGCTTTTCTGCTCATCATCTCTGCAACGGGAGATCAACCAACAGCGCCCTGTGCGGA
 ATGACCTCTGTGCCCTGSAATGTGGATCCCCAAACACTTTGGGCTTTTCTAGCGCATGGGCAACAGCCCTGATGA
 TGGAGGGCTCTCTAGTGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACCATCTGCTTATGT
 ACATGATCGCGGAGCTCTGATGCTGAAGCTCTACCAAGCGGACCCCGGACATCAACCGCAGCGCTTACAGTG
 CACTACGCTCTGCGCATCTGTGCTCTTTCTCTGTGCTGGGGTGTGCTTTTGGCAAGGGAACACCGGCTTCT
 GSAATCTCTTCTCCATCATTCACATCATCGCCACCCTGCTCCTCAGCAGCGAGCTCTATTACATGGGCGGTGGA
 AACTGGACTCGGGGATCTTCCGCGGCATCTTCCACGTGCTTACACAGACTGCATCGGCACTGCTCCTTTACTTTCGCTTCTACA
 TCACTCATGAAGCTCCGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGACACTCCGTGGTCT
 GGGCTCTCGCGCTCTTCTTCTTCTTCCAGGGACTCAGCACTGGCAGAAAAACCCCTGAGAGTCCAGGGAGCACA
 ACCGGGACTGCATCTCTCGACTTCTTTGACGACCACGACATCTGGCAGTCTCCTCTCCTCCATCGCCATGTTCG
 GTTCTCTCTGGTGTGTGACTGACATGGATGACGACCTGGATCTGTGCAAGCTTGGATCTATGTCTTCTAGC
 AGGAGCTGGGCGCTTCTGCTTCACTCAAGGGGCGCTGAGCTCCTTTGTGTATAGAACCGGTCACTCTGTCTGCT
 GTGCGGATGATCCAGCCGCTGCCAGCACTGGATGGCAGCAGGACCGAGTCTAGCTTAGGCTTGGCGCT
 GGGACAGCATGGGGTGGCATGGAACCTTGCAGTGCCTCTGCCAGGAGCAGGCTGCTCCCTTGGAAACCC
 AGATGTTTGGCCAAATGCTGCTTCTTCTCAGTGTGGGCGCTTCCATGGGCGCTGCTCCTTTGGCTCTCCATTT
 TCCCTTTTGCAGAGGAAGGATGGAAGGACAGCTCCCATTTTCATGCCCTGCATTTTGGCGGTCTCTCTCCC
 ACATAGCCCCAGCTGGGACCTAAGGCTCTTTTCTCCCATACTCCCACTCAGGGGCTAGTCTGGGGCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGTGCTCCCTGGCTGCCATCACTGCCCATTCAGTCAAGC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTTGGCGAGTGGTGGCAGACTTTTGGTGTCAAGGCTGCAAGGG
 CTTGGGGCAGTGGCTATTCTCTTCCCTCTGACCTGTGCTCAGGCGTGCTTATTGCAATGCGCTCAGCCCAATT
 TATGAACCGCTTCTGATTCAAGAGGCTGAATCAGAGGTCAACCTCTCATCCCATCAGCTGCCAGACTGATGCC
 AGCACCAGGATGGAGGGAAGAGCGCTCACCCCTCCCTTCTTCTTCCAGGGCCTTACTCTTCCCAACCC
 AGCTGTGGGCTTCTCAGTGCAATGTGACTGCCACGAATGTCAGAGGCAAGAGGAGATGATCAGATTTCAG
 CCGGTCTGCTCTCCAGCTGTGGGACCCCACTGCTCACTTGAAGAGGCGCTCAGGAGAGGATGTCTGTTT
 CCTCTAGTGCCTCAGCTCTAGGCTCCTTAGGACCCAGGCTGGCTCTAAGTTTCCGCTCAGTCTTCAGGCA
 AGTCTGTGTTGATCATGCCACACATCTTATGAACCTTGCAGTTTACAAGAATTCGCCAGCTCTGGGAC
 CTTGGCCACCTGGTCTGTGATACCTCTCTGCTCCACTGCTCAGCCAGATGCTGAGGATGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGGAATGTGTTTTCTCCAAACTGTTTTATAGCTCTGCTTGAGGGCTGGG
 AGATGAGTGGGCTGGATCTTTCTCAGAGCGCTCTCCATGCTAGTGTGATTTCCGTTTCTATGAATGAAT
 TGCATTCAATAAACACCAAGACTCAAAAAA

10006768.120601

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAATVQRKDFPSNSFYVVVV
VKTEDQACGGSPLFPYFPAEDEPVDQGHRKQTLVSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPEGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSTYGYQGRSFEPVGTTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFNWNIATIAVFYALPVVQLVITYQTVVNVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPNTNFQFDTSMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFS
VLGVVFGKNTAFWIVFSIIHIIATLLLLSTQLYYMGWKLDLSGIFRRILHVLVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

10006768.120601

FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGCTTTGGGCGTGGAGGGCCTGTCTCTG
 ACCATGGTGCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAACTATGGTGGAAATTTCCCTTTTATACC
 TGACCAAGTTGCCGCTGCCCGTGGAGGGGGCTGAAGGCCAGATCTGCTGTGTCAGGGGACTCA
 GGCAGGCCAACTGAGGGCCATTTGCTATGGATCCAGATTTGCTTGGCTTCTGCTGGTGACTGAC
 GGCCCTGGAGCCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGCTCCACAGCCTGTGCTTGTGACGCTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACACGGCCTGGCATCCC
 CTTCTCTTCTTGTAGGCTTCAGACCGGGATGAGCCAGGCCACGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCACAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAACTCTCAAAGTCTTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT
 GCACATACCTCCAGGAGCCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCTTGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGTGATGGATGAGAA
 TGACAACGTGCCCTATCTGCCCTCCCCGTGACCCACAGTCAGCTCAGTCCCTGAGTCCCAAC
 CAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTGAAGGGGAGAGCCTTCA
 GGTGGAGCCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCAGCAGGCCCAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGACGTGT
 GAAGTCGAAGTCCAGTCCAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCCGGACTCTGGTGGCCATGTCTAACAGCCA
 TTGATGCTGACCTCGAGCCCCGCTTCCGCTCATGGATTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGGCCACGCCACCGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATCTCCGGGGAGGTGCACACC
 GCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGTGTTGGAGGCCCCAGGA
 TACAGCCCTGACTCTTGCCCTCTGTCCTCCCAATACCTCTGCACACCCCGCCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCAGTGGGACCGTCCCTACAGC
 TTCACCTTGGTCCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCTTACCTCACCCTTGCCCTGCATTGGGTGGAGCCAGTGAACACATATCCCCGTGG
 TGGTCAGCCACAATGCCAGCATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTCGCTGCAAC
 GTGGAGGGGACGTGCATGCACAAGGTGGGCGCATGAAGGGCATGCCACAGAGCTGTGCGGC
 AGTGGGCATCCTTGTAGGCCCTTGGTAGCAATAGGAATCTTCTCATCTCTATCTTACCCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGGCCCTGAAGGGC
 ACTGTCGAATGGCCCGAGGAGCTTAGCTGGGAGCTTGGCCCTTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCAGCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGACCTCCATC
 CTGCCCCTGGGTGGAGGACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGGCCCAATATAAGGCCCA
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAGGAAAAAAGG

FIGURE 132

MVPAWLWLLCVSVQPALPKAQPAELSVVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGRTPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDPMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFVEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLEHLVLMVDENDNVPCPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAFOVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAPPSHEVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLTALHWVEPREHIIPVVVSHNAQMWQLLVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLILIFTHWTMSRKKDPQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

10006758-120601

FIGURE 133

CCGGGGACATGAGGTGGATACGTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAATCTCCCTCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTGAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCAGGGCTTAGAGTACGCAGTGACAATGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATTCCTTGAAGCTATTACACAGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAACCAGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCCGTTGGCTGAATGCAGGCATCCATTCGCCAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTCTTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATATCAAACTCAAAACCGATTATGGAGGAAGACGGCGTCCCGAAATC
 CTGGAAGCTCCTGCATTTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAAACCTTGCTCCGAAAGTGACCATGGACCCACGCCAATTCGGAAGTGGGA
 GGTGAAATCAGTGTAGATTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATCATCATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTCTGTGTCGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAAACGGCATCAAAATTTGCATTTCAGTTCAGTTGAGTTGAGAGTACGGGACCTATGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGGCAACCTCTACTAGCGCATGGCTCTGCTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTTCCATACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCCTGGCGGTGCTCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGTGGCTGGGCGGCTGCACTC
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGTCTCTGGTGGCAAT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTTCTTTAATTTTC
 TCGCAGTCTTCTGGAAAAATATTTTCCCTTGAGCAGCAAACTCTTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTTTGGCC
 CAGGCTGGAGTGTGAGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA
 ATTCTCCTGCCTCAGCTCTTGTAGTAGTCTGGTTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGCTCAAACTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTAGGCCACTG
 TGCGGGGCCGTCCCTCCTTTTTTATAGGCTGAATACAAAGTAGAAGATCACTTTCTTCTC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCTCTCTTCCCTTTGTTATTACAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGCTACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 TGACCATCTAAATTCAGGATGGTGAATATCCCATCTGTCTCTAATGGGCTTACCTCTCT
 CTTTGGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGCTCTAATCACTACT
 CTGGCCTGGATAATCTCACTGCCCTGGCACTTCCCATTTGTGCTGTGTGTGTGTGTGTGTGT
 TCCTTGTCTCTGGTTTGT
 TCTGTCTATTTGTATCCTGGACCACAAGTTCTTAAGTAGAGCAAGAATTCATCAACCAGCT
 GCCTCTGTTTCTTTTCACTCTCAGCACGTACCATCTGTCTTTGTTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFI DLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

10066768-120601

FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAAATG
 GCATCTTACCTTTATGGAGTACTCTTTGTCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC
 CCCGGCCAATGCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC
 AGGTGATATTCCCTCAACACCGACTTTGCCTTCCGCCATATACCGCAGGCTGGTTTTGGAGACC
 CCGAGTCAGAACATCTTCTTCTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT
 TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCAGGGCCTGGGCTTCAACCTCACACACA
 CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCACAGC
 AAAGACCTGACCTTGAAGATGGGAAGTGCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC
 AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
 ACCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCAAGGGGAAGGTT
 GTAGACATAATCCAAGGCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT
 TAAAGCCAAAGTGGGAGAACCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCCTGG
 TGGCGAGCAGGTCACGTGTGCAAGTCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG
 GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT
 CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC
 TGATAAAGTGGAGCCACTCACTCCAGAAAAGTGGATAGAGGTGTTTATCCCCAGATTTTCC
 ATTTCTGCCTCCTACAATCTGGAACCATCCTCCGAAGATGGGCATCCAAAATGCCTTTGA
 CAAAATGCTGATTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC
 ACAAGGCTGTGCTGGATGTGAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG
 TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT
 GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTCTAGGGAAAGTGAAAATCCCA
 CTAATCCTAGGTGGGAAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAA
 CAAACCACATCCCTCTTTCTGTCTGAGGGTGCATTGACCCAGTGGAGCTGGATTGCGTG
 GCAGGGATGCCACTTCCAAGGCTCAATCACCACCAATCAACAGGGACCCAGTCACAAGCC
 AACACCCATTAACCCAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAAGTACGTTTCATG
 GGATGTTGCTGGGTTACCATATTTCCATTCTTGGGGCTCCAGGAATGGAATACGCCAAC
 CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAATATGAAT
 TCAA
 AAAAAA

10006768-120601

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKEQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSK GKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGI AKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

10006768:120301

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCG
 CTGAGTCCAGATTTCTTCCCAGGAACACAAACGCTAGGAGACCCACGCTCCTGGAGACACCAG
 CCTTTATCTCTTCAACCTTCAAGTCCCTTTTCTCAAGAACTCCTGTGTTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGGCCACAAAGAGACAGATGAAGATGC
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAAGACCTCCAATGGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGC
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCACTCCAGTGGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCCAG
 TGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT
 TCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGCAA
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTTGGTCTCGGTTGTGGCG
 GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
 CTTTAACACAGCTGTCTACCACCTCATGGCCTCAACCATGGCCTTGTTCAGGCCCTGGAG
 GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCTCAACTGGTCTGGAGGAGACCAAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGGCCCTGAGCAGCCCCGGAAGCAAG
 TGCCGATCTTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTTCAATTCATC
 CCAGGAGACCCCTCCAGCTTTGTTGAGATCCTGAAATCTTGAAGAAGGTATTCTCACC
 TTTCTTGCTTTTACCAGACACTGGAAGAGAATACTATATTGCTCATTTAGCTAAGAATAAA
 ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG
 CTTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSA NTGSSVSSGASTATNSGSSVTSSGVSTATI
 SGSSVT SNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
 SNGAGTATNSESSTTSSGASTATNSDSSSTVSSGASTATNSESSTTSSGASTATNSESSTSS
 GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTTSSEAST
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVA VGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
 GPGGNHGA PHRPWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

1006768.12601

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGCTTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGAAGGAGC
 TGCAGAAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTGCGCGTTGTCACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

100673.12601

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGLSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

100675.12661

FIGURE 141

CTCCGGGTCCCAGGGGCTGGCCGGGGCGGGCTTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCCGGGGGGCGATGACCTGTGCGCTGACCTGACTCACTCCAGGTCCGGAGGGGGGGGGGGGGGGGCGGACTCG
 GGGGCTGGCCGCGGGGGGAGCTGCCCGGTGAGTCGGGCGGAGCCACTGAGCCCGGAGCCGGGGACACGCTC
 GCTCCTGTCTCTCCGAATGCTGCGACCCGGATGGGCTTGAGGAGCTGGCTCGGCCCCACTGGGGCGGCTCGCC
 CCTCGGCCACCGCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCGAGCCCGCCCTCCGACCTGGGCGCTGAC
 CCCCGGATCAGCTGCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGTGAACATCTCCAACATAC
 ACAGCCCTTCTGCTGAGCAGGATGGCAGGACCTGTACGTGGTGCTCGAGAGGCGCTCTTTGCACTCAGTAGC
 AACCTCAGCTTCTGCGCAGGCGGGAGTACAGGAGCTGCTTTGGGCTGCAGACGACAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGSCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCTGCGCTCAGCGGCACTCAC
 CTGTTCACTGTGGCACAGCAGCCTTCAAGCCCATGTGTACCTACATCAACATGGAAGACTTCAACCTGGCAGG
 GACGAGAAGGGGAATGTCTCTCTGGAAGATGGCAAGGGCGGTTGCTCCTTCGAGCCGCAATTTCAAGTCCAATGCC
 CTGGTGTTGATGGCAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGGCAATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCTCAGCCTAC
 ATTCTGAGAGCTGGGCGAGCTTGAAGGCGATGATGACAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTCTTTGAGAACACCATTTGTGTCCGCTATGCCCCATCTGCAAGGCGATGAGGCTGGAGCGAGCGGTG
 CTACAGCAGCGTGGACCTCTCTCTCAAGGCCAGCTGCTGTGCTCAGCGCCCGACGATGGCTTCCCTCTCAAC
 GTGCTGAGGATGTCTTCACTGTGAGCCCCAGCCCCAGGATGGCGTGAACCCCTTTCTATGGGCTCTTCACT
 TCCCACTGGCACAGGGGAAGTACAGAGGCTCTGCGCTGTGTGCTTCAACAATGAAGATGTGACAGAGACTTCA
 AGCGGCTCTACAGGAGGCTGAACTGAGCCTGAGACACAGCTGAGACAGTGGTGAACCCCTGGGCGCCACCCCGG
 CCTGAGGCTGCTACCAACAGTGCCTGGGAAGGAAGATCAACTCATCCTCGACCTTCCAGACCGGCTGCTG
 AACTCTCAAGGACCACTTCTGATGGACGGGACGCTCGAAGGCGATGAGGCTGGAGCGAGCGGTG
 TACCAGCGGTGGCTGTACACCGCTCCTGGCTGCAACACACCTACGATGTCTCTTCTGGGCACTGGTGAC
 GCGCGCTCCACAAGCAGTGAAGCTGGGCGGCTGGGCGGCGGCTGACATCATGAGGAGCTGACGATCTTCTCATGGGA
 CAGCCGCTGCAGATCTGCTCTGGACACCCACAGGGGGCTGCTGTATGCGGCTCAACTCGGGCGGTAGTCCAG
 GTGCCATGGCCAACTGCAAGCTGTACCGCTCTACAGCCTCAGCTGGCCACCGGATGGATCGAGGACATGAG
 GGAGCGAGCGCAAGGACCTTTGAGCGGCTCTTGGTGTGTCCCGCTCTTTGTACCAACAGGGGGAAGGCCA
 TGTGAGCAAGTCCAGTTCCAGGCCAACAACAGTGAACACTTGGGCTGCCCGCTCTCTCCAACTCGGCGACCCGA
 CTCTGGCTACGCAACGGGGCCCCCGCTCAATGCTCTGGGCTCCTGCCACGTGCTACCCACTGGGACCTGCTGCTG
 GTGGGCAACCAACAGCTGGGGGAGTTCCAGTGTGCTGCTACAGAGGAGGCTTCCAGCAGCTGGTAGCCAGCTAC
 TGCCACAGAGGTGGTGAGGACGGGCTGGCAGACCAACAGATGAGGTTGGCAGTGTACCCGTCAATATCAGCACA
 TCGCGTGTGAGTGCAACAGCTGGTGGCAAGGCCAGCTGGGTGCAGACAGTCTACTGGAAGGAGTTCTTGGTG
 ATGTCCAGCTCTTTGTGCTGGCGGTGCTGCTCCAGTTTATTTCTTGTCTTACCGGACCCGGAACAGCATGAAA
 GTGCTCCTGAAGCAGGGGGAATGTGGCAGCTGCAACCCCAAGACCTGCCCTGTGTTGTCGCCCTGGAGCCCG
 CCACTCAACGGCTTAGGGCCCCCTAGCACCCCGCTCGATCACCAGGGTACAGTCCCTGTGACAGAGCCCCCG
 GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCTGGAGGATATCCCACTG
 TGCCCCCGCCCCGGGTCTCGCTTGGCTCGGAGATCCGTGACTCTGTGGTCTGAGAGCTGACTTCCAGAGGACG
 TGCCCTTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGCTCACTGGACCTCCCTGCTGTGCTCTTCTGTGGAAC
 ACGACCGTGGTGGCCCGGCTTGGGAGCCTTGGAGCCAGCTGGCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCCACAGACACCCCAACAGCGCTGGCCCGAGAGTCTTGGCCAAATATGGGGGCTGCTTGGTGTGGTGGAC
 CAGTGTCTCTTATGTAACTGAGCCCTTTGTTTAAAAAAACAATCCAATGTGAAACTAGAATGAGAGGGAAGAG
 ATAGCATGGCATGCGCACACACAGCTGCTCCAGTTTATGGCTCCACAGGGGCTTGGGGATGCATCCAAGTGG
 TTGTGTGAGACAGATTTGGAACCTCACCACCTGGCCTCTTCACTTCCACATTTATCCCGCTGCCACCGGCTGC
 CTGTGCTCACTGAGTTCAGGACAGCTTGGGCTGCGTGGTCTGCTTGGCACTGAGCCAGGATGTAGTTG
 TTGCTGCGCTGCTCCACCACTCAGGACCGAGGGCTAGGTTGGCACTGGCGGCTTCAACAGGTCCTGGGCTGC
 GGACCCAACTCCTGGACCTTTCCAGCTGTATCAGGCTGTGGCCACGAGAGGACAGCGGAGCTCAGGAGAGA
 TTTCTGTCAATGTACGCTCTTCCCTCAGAATTCAGGAAGAGACTGTGCGCTGCCCTCCCGTGTGTTGGTGA
 GAACCGGTGCGCCCTTCCCAACTTCCACCTCGCTCCATCTTGTACTCAACACGAGGAACCTAAGTCAACC
 CTGGTCTCTCCCACTGCCAGTTCACCTCCATCCTCACTTCTTCCACTCTAAGGGAATACCACTGCC
 AGCACAGGGGCCGTAATTTCTGTGGTTTATACATTTTTTAATAAGATGCACCTTATGTCAATTTTTTAATAA
 GTCTGAGAATTACTGTTTAAAAAATAA

1006768.120671

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFRLR
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLLEDGKGRCP
FDPNFKSTALVVDGELYGTGTSSFGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETOQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGHHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSFVPTGEKPCQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASICYPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYKFEFLVMCTLFVLAVLLPVFLFLYRHRNSM
KVFLKQGECAVHPKTCPPVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRP
PLSIQDSFVEVSPVCPRPVRVLGSEIRDSVV

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Transmembrane domains:

amino acids 23-46 (type II), 718-738

10006768.120601

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCGTGCGAACCGA
 CCGCAGCCAGCGCGGAGGAGCGGGCAGGGCGGGGACGGGAGCCCGGAGCTCGTGTGCGCGCGCGCGTGTGCGCGTGC
 TGGCCGCCCGCGCTCCCGCGCGGAGCGGGAGGAGCGCGCGCACCTCGCGCGCGGAGCGCGCGCTTAGCGCGCGC
 CGGGCATGGTCCCTCTTAAAGGGCAGGGCCGCGCGCGGGGGCGGGTGTGCGGAACAAGAGCGCGCGCGGGG
 CTTGCGGGCGCTCGGGGCGCGCATGGGCGCGCGGGCGCGCGCGCGCTGCCCGGGCGGGCCTCG
 CGGCGCTAGGGCGGGCTGGCTCTCGTGGGCGGGGCGAGCGGGCTGAGGCGCGCGCGGAGCTGCGGGCGGGCGGG
 GCGCGCGCGCGCGCGCGCGCGGAGCGGGCGGGGCA**ATGG**CGCGCGCGCGCGCGCGCGCTGCCCGGGCGGGCCTCG
 TGTCTCGGCTCGTCTGGGCTTGTCTGGCTCGGGCTCGGTCTGCCCCGGGCTTCGAGCTGAAGCGAGCGG
 GCGCCAGCGCGCGCGCGCGCGCGGGCTCGGCTCGCGGACGGCGCGGCTTCCGAGCGCGCGCGCGCGCG
 CGGATCGCGCGGGGCGAGCTGTGGCGCGCGGGCTCGGACCCAGATGGCGGGCGCGCGCAGAGAACTTTCTCT
 TCGTGGGAGTCATGACCGCCCAAGAAATACCTGCAGACTCGGGCGGTGGCGCGCTACAGAACTGTCTCAAGACA
 TTCTCTGGAAAGTTCAAGTTCTTCAAGTAGGGTTCTGACACATCTGTACCAATTCAGTAGTGCCTACGCGG
 GTGTGGAGACTCCTACCGCGCCAGAGAAAGTCTTCATGATGCTCAAGTACATCACACCACTACTCTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGCTCGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCGCTCTTCTTGGGCAGACGGCTGGGCGACCAAGAAATGGGAAACTGGCCCTGG
 AGCCTGGTGAAGACTTCTGATGGGGGGCTTGGCGTGATCATGAGCGGGAGGTGCTTCGGAAGATGTGCGCGC
 ACATTGGCAAGTGTCTCCGGGAGATGTACACACCCATGAGGACGTACCATATACCCCAAAACCCACCTTCCAGT
 CAGGGGTCCAGTGTCTGCTGTTTATGAGTAGCGGCAGCTTTTTATGAGAATACAGCAGAGAAAGAGGGT
 ACATTAGAGTCTCCATAAGCTTAATACCAAGCTATCACATACCCCAAAACCCACCTTCCAGT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGCACATAACAGTTCGACGCGAAA
 TTCTCTCATGACCAATACAGACACAGAAATTCATAAAGGAGACTCCAGCTGGGAATCCCTCCCTCTTCA
 TGAAGTTTCAGCCCGCGCGCAGAGGAGATTCTGGAATGGGAGTTCTGAGTGGAAATCTGTATTCCGAG
 TTAGCGGGCCCGCCCTCGAAGAGCAATGGACTCCGCGCAGAGGAGAGCTTGGACGACATGTGATCGAGGATCA
 TGAGAGATGATCAATGCCAAGCCAGACAGGAGGCGCATCTGACTTCAAAGAGTTCAGTAGTGCCTACCGC
 GGGTGAACCCCATGTATGGGCTCAGTACATCTTGAGACTTGTGCTCTGTACAAAGAGCAAGAGGAGAGAAA
 TGAACGCTCCTGTGAGGAGGCGCGCTTTTACAGCAGACTTCAGCAAAATCAGTTTGTGGAGATGAGGAG
 TGATGTCACAGAGTTTGGCCAGAGAAATCAATCAGGAATCTGGATCTTGTCTTCTCAAATCCCTCGAAGA
 AGCTCGTCCCTTTCAGCTCCCTGGGTCGAAGAGTGAACAAAGAACCCAAAGATAAAAGATAAACAATCTGA
 TTCTTTTGTCTGGGCTTGTGACATGTTTGTGAGATTATGAGGAATCTTGAAGAAGCGTGTCTTATCCCAATC
 AGAAGCTCAAGCTCGTGGTGTGCTTTCAATTCGACTCCAAACCTGACAAGGCCAAACAAGTTGAATCATGA
 GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTCGCTGTGTCTGGAGAGTTTTCAGAGCGCTGG
 CCTCGGAAGTAGGATCTCCGAGTTTAAACAATGAATCTTGTCTTCTCTCGACCTCGACCTCGTGTTTACTA
 CAGAATTCCTTCAGCGTGTGCAGCAAAATACAGTTCTGGGCCAAACAATATATTTTCAAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATGTGCGGAAAGTTCCGAGTGAACAACATTTTGCCTTACTCAAGAAATGAGTCT
 GGAGAAATATGGGTTTGGCATACGCTGTATTTATAAGGAGATCTTGTCCGAGTGGGTGGCTTGTATGTTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTCAACAAGGTTGTCCAGGCGAGTTTGAAGACCTTTAGGAGCC
 AGGAAGTAGGAGTAGTCACGTCACCATCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAATGT
 GCTTGGGCTCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCC**TAAT**GTCCAGCTTGTGCGAAAGACGTTT
 TAATTATCTAATTTTATTTTCAAAAATTTTTGTATGATCAGTTTGTGAAGTCCGTATACAAAGGATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCCTTAAGATTGAGCTTCTGAAACAAGAGGTGATCAGTGTGTGCTTTGAA
 CACATCTCTTCTGTGCAACATTATGTAGCAGACCTGTTAACTTTGACTTGAAGTGTACCTGATGAACAAACTTT
 TTTAAAAAATGTTTTCTTTGAGACCGTTTGTCTCAAGTCTTATGGCAAAACGTTGAACATTTCTGCAAAAGTAT
 TATTGTACAAACAGCTGAACCTCGGTAAGTCTGTGTTGATGTTAACTTCCACAGATTCTTCTGCTTTGTG
 GTTTGTTTTTTTTTTTACATTTGTTTAAAGCCATTTTCATGTTCCAGTTGTAAAGTAAAGAAATGTGATTAAT
 GCTGTTTCATCATCTTCTCAGGAGGCTTCCAGAGTGTGATCATTTCCTTCTCATGTGACTCTGTCTAGACTGGC
 CAGCTAGTGTTTTGTGTTTGTGTTTGTCTTTTGTGAGACGAGTCTCACTCTGTTACCCAGCGCTGGAATG
 CAGTGGCGCAATCTGGCTCACTTTAACTCCACTTCCCTGTTCAAGCAATTCCTCTGCTTCCCTCCCGAGT
 AGCTGGGATTACAGGACACACACCCAGCGCCAGNTAGTTTTTTGTATTTTTAGTAGAGCGGGTTTCCACAT
 GCAAGCCAGCTGGCCCACTAGGTTTAAAGCAAGGCGCGTGAAGAGCGCAGTGAAGTATGGTGTCTCTGCT
 TGGTATGTTTCATTCGGCTTAATAGACCTGGCATTAATTTTCAAGAAGGATTTGGCATTTCTCTTCTGACCTT
 CTCTTTAAAGGGTAAAAATTAATGCTTTAGAAATGACAAAGATGAATTTATCAATAAATCTGATGTACACAGACT
 GAAACATACACACATACCCCTAATCAAAAGCTTGGGAAAAATGTGTTGTTTTGTTCTTCTACCTGTCTG
 TGTATGTGGTGGAGATGGTTTTCACTCTTTCATTACTGTTTTGTTTATCCTTTGTATCTGAAATCACTTTAA
 TTTATTTAAATATCTGTTGTTCAGAGCTGTCATTTCTTGATACCTGTTAGTTATGTTATTTAGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTCAGTAACCCGATCTCCAAGATTTTCTTTTGGAAACGCTTTTCCCTCTC

10006768.120601

FIGURE 143B

TTAATTTTATATTCTTACTGTTTACTAAATATTAAGTGTCTCTTGACBAATTTGGTGCTCAIGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCACAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCAATGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCAITTTGAAAAATAAACCAAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAAAGTTAAACACGAAAAAA

1006768-120601

FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPEGENFCMGGPGVIMSRVLRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPKDKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQVNLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEVDVLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMC LGSKASTYGSTQQLAEMWLEKN DPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

1006768.120501

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGT
 ACGGACGACGCC**TATGA**AGCCCTTAGTCCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTCATGTCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTGAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
 TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGTACAGTATTCATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
 TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGGTTCAGGAAAAA

1006768-120501

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPPMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

1006768-12664
10021-2929000

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCC TG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTTGTGTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTCAAGACA
 GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCCCTGAGACCAGTGCAGAGGCTATGGAAGTGC GGTTCTTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTCTAAGGC
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCCAGATTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCAT
 CGTGGGATATGTTGACGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGTGAGCAGAGTCATGAGGTGGAATCCAAGGTATGTATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGAAAAATCCA
 GCGGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCCCTCAGACTGACAACAGAAATTTGTATTTTAC
 ATTTCAATCCCCATTTTATCAGCCTCCCCCCAGCACCCCTCTTACACGAGTAGGGGGCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCACTTTGAAGGCTTGTGTAGACCCATATATCCAGCATGCGATGTATGACGA
 GGGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTTGGGGAT**TG**AGACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGATCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGTCCTCATTTGCTAGTCAACGACAGTGATTCTTGCCTCACAGGTGAAGATTAAGAGA
 CAACGAATGTGAATCACTGCTTGCAAGTTTGAGGGCACAGTGTTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCCACCAATAAACTCTGTTTGCCTTATCCACATTAATTTTACTTTTCTCTA
 TACCAAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTCTACTGATTCTATAAGCCCCAGCATTAACGTATACCAAAACAGGCCAAG
 AAAACAGAAAGAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTTAAACAATTAACATAACAATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTTGTGCCCAAAATGCAGAGTTGGTTTTAATATTTAAATATCAACCAGTGTAATT
 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

1006768-120601

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGFGQQLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**AATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAAGAGACCTACAA
 TTACTATAGCACATTGTCATTTACAACGACAAACATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCTACTGAGGATCCTGAAACTGTAG
 ATAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAAATAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAATGAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAAACCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAGCCTCATGGAACAGATAACATTTTTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAAATGGAGAAGACTTGCAAAACAGCTAGATTGTAGTGCATCTAATAAAC
 TGTTTGCTTGATGCATGTATTTTCTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTTCATTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTCCCTC
 AGCTCCTCTCATTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTTCATTATGAAGGTCAAGCAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAGAAGCCAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

1006758.120601

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTINYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSFPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

10006768-126601

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCTCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCCGATTGCCG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCTCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCCTTCGGGCCTTGACGCCCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
 GGCCGTGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCATGCTGGGGCTGCCCGCGCCGAGCCGCCCGGAGCCGCAGGGGCGCTCTGA
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCAG
 GCTCCAGGGCCACGGCGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAAAGTCCGGTACTT
 GGCGCTTTGTTTCTGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTTA
 AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

1006763-126601

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLIVHAAVGVGTALALLSCAALVWHFCLRDWGCPRRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

1006768.120601

FIGURE 153

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCGCATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGCGGGCGTGGGGCACCAGG
 CCCAGCGCCGACGATCGCTGCCGTTTGGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGG
 TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATTCGGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGG
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATTGCTGTTTGCCTGTTTCTTATCAT
 TGTGGGATGTTAGGATATTGTGGAACGGTGAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGGCTTGTCAATTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGCCCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCTTTTGAAGGAACCAAACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAATCTCGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAGAAAGATGTCACAGAAGAAACCAAACTGTTTATTTGGACTTGTGAAT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCTAATAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTGGAGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACATAA
 ACTTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAAATATATATCAGAAAACCTTT
 AATATTGGTGACTACCTAAATGTGATTTTGTGCTGTTACTAAAAATTTCTTACCACTTAAAA
 GAGCAAGTAAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGCTGTGTTAAA
 TCTGTATAAATCAGTCGATTTTCACTTCTGATAATGTTAAGAAATAACCATTATGAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTTGTAGCCTTTCTGTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTGAGAAATGATGCTGGCTTTAGGAAGTATTAATA
 GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTCTCCCAATG
 AAGACTCTTTTGCACATAAACACTTTTTAAAAAGCTTATCTTTGCGCTTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATTCTTTGTTTTATTCTACTGATTA
 ATATACTGTGGCAAATTACACAGATTATAAATTTTTTACAAGATATAGTATATTTATTT
 GAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTTTTGTTTATTTCTCAGAAATATGGA
 AGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTILTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

1006758-120641

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACCTCGGGCCTCCTCCAGCCAGTGTCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATGT**TACAGGATCTTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGTCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAGAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGGCCAGACCAGGATCTGGA
 TGTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCGT
 GTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGGCCTTGCGAGGTCAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTACCAGAGAAGA
 TGATGTGTGACGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCT**GTAA**TGCTGCTGCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTCTG
 CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
 CTCGCCCCACAGCCTCAGCATTCTTGAGAGCAGCAAGGGGCTCAATTCTGTAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCC
 AGCATCCCAGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTTCCCACTACTGAATGAAGCAGGCTGTCTTGTAAAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGCLSGSLVSL
HCLACGKSLKTTPRVVGGEEASVDSWFPQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSSGGLPMYQSDQWHVVGIVSWGYCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

1006753-120601

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATGG**CCCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCTGGGCC
TTTTCTCTTCCAACCTGCTTCACTGCTGCTGCCAGCAGCAGCCGCGGGGAGGCGGGCAGGGGCCCATGCCA
GGGTGAGATATGCGAGGGATGAACGTAGGGCACTTAGCTTCTTCCACGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGTGAAGTAATCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
ATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTA
AGAAAGAGAGCAATGAGACACAGTGTTCACCTCATCCGTGTCCTGGTTTCTTACAATGTACCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAATTCAGATTCTACCTGTTGCCCATCTCGG
AGGACAAGGTCTGGAGGGAAAAGGCCAAGCCCTTTGACCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACTTCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCCAGC
CTGTCTCAAGACCGACAACCTTCCTCCGTGGCTGCATCATGACGCCCTCTTTTGGCAGCCATCCCTTCGACCC
AGGTCGTCTACTTCTTCTCGAGGAGACGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGAATGACGTGGGCGGCCGAAAGCTGCTGCAGAAGAAGTGACACCATCTCTGAAGGCCCAGC
TGCTCTGCACCCAGCCGGGCGAGTGCCCTTCAACGTCACTCCGCCAGCCGCTGCTGCTCCCGCGATTCTCCCA
CAGCTCCCCACATCTACGCAGTCTTACCTCCAGTGGCAGGTTGGCGGGACCGAGAGCTCTGCGGTTTGTGCC
TCTCTCTCTTGGACATGAACTGTCTTTAAGGGGAAATACAAAGAGTGAACAAAGAACTTCAGCTGGACTA
CTTATAGGGGCCCTGAGAACACCCCGGCCAGGCAAGTGTCTGAGTGGGCCCTCTCTGATAAGGCCCTGACCT
TCTGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA
CAGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTGATGTACCTGGGAACCCACAG
GGTCCGCTCCACAAGGCTGTGGTAAAGTGGGACAGCAGTGTCTGATGGTGAAGAGATTACGCTGTCTCCGTGACC
CTGAACCTGTTCGCAACCTGACAGTGGCCGCCACCCAGGGTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCGCCAGGCCACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCACTGTGCT
GGGACCTGAGTCCCGAACCTGTTGCCCTCTGTCTGCCCAACCTGAACCTGATCTGGAAGCAGGACATGGAGCGGG
GGAACCCAGAGTGGGCACTGTGCCAGTGGCCCATGAGCAGAGCCTTCGCGCTCAGAGCCGCCCGCAATCATT
AAGAAGTCTGCTGTCCCACTCCATCTGGAGCTCCCTGCCCCACCTGTACGCTTGGCCTCTTATTATT
GGAGTCTGGCCAGCAGCAGTCCAGAAAGCCTCTTCACTGTCTACAATGGCTCCCTCTTGTGATAGTGACAGG
ATGGATGGGGGTCTCTACAGCTGTGGGCACTGAGAATGGCTTTACACCTGTGATCTCTCTACTGGGTGG
ACAGCCAGGACCAGACCTTGGCCCTGGATCTTGAACCTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGCCCCACTTTGTGACTGTCACTGTCTCT
TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGG
TTGAGGCTGTGAGACCTCGGCCCTGGGAGAAGGCCCGTTAAGCAGAGCAACACACTCCAGTCTCCCAAGG
AATGCAGGACCTTGCAGTGTGAGCGCTGACAACTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA
CAGGCCGGGGTCTGCGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCAGCCCTGACTAGGATGACAG
CAGCAGAAAGACCACTTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC
CCCCAGACTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCTCAGTTCTGGCCATTCCAGGACCCCTC
CAGAAACACAGTGTCTCAAGAGACCTAAAAAAGCTGCCTGTCCAGGACCCATGGTAAAGAACACCAACATC
TAAACAATCATATGCTAACTGCGCATCTCTGAAACTCCACTCTGAAGCTGCGGCTTTGGACACCAACACTCCCT
TCTCCAGGGTCACTGAGGAGTCTGCTCCCTCTGCTTCCCTTACAGTCTGTCACCGCTGACTCCAGGAAGTC
TTTCTGAGTCTGACCACTTCTTCTTCTGCTTCAAGTGGGGCAGACTGTGATCCCTCTGCGCTGGCAGATGG
CAGGGGTAACTGAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTCACTCTCCCTTCCCTTTCTTGT
TTTGGGATTAGAAAAGCTGCTTGTGACAGACTGTTATTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
 ><subunit 1 of 1, 761 aa, 1 stop
 ><MW: 83574, pI: 6.78, NX(S/T): 4
 MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
 FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFPDPAHKHTA
 VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAPSTQVVYFFFE
 ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
 PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
 NPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
 YLGTTTGLSKHAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
 CSVYESCVDCVLARDPHCAWDPESTRCTCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
 QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIQDGVGG
 LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVVKVPLTRVSGGAALAAQQSYWP
 HFVTVTVLFAVLVSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
 SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

1006763-120601

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGC**ATGG**GCTGGGCGAGCGAGTGCTTCTTCTAGTGGGCTTCCCTTCCCTGGGGTCCCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAAACCAAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCCTTCTGGGAAGAACTTAGG
 TGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAGAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTTCTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
 CAGTATTCGGTTCCCTTGTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCATGCAGTACATTTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTCTGACTTTGCGCTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAAAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGC
 CAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTGTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAATGTGAAAAATTTGGGA
 CTGGCTTCCCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGCTGTGTTTGTACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTACAGTT
 AAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAAGAGAT
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGGCGCAGCCACCTCAAGCCCTA
 TGTCTTTAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACAT**TA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCACATTGC
 TAATTTTGTACAAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT
 CTTGTCTCCTTTGTTTGGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCACTGACCTTCAGATTCCAGCCTTAAAAATCCACCTTCCCTCTCATGCGCCTCTCCGAA
 TCACACCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGATCATTTCTTTCAGTTTCTGTTT
 TGTCTTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCGCTTGCTTGAGAGTTTGAGGCG
 CGGACACAGGCTCACAGGCTCTCCATTTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGATGGAGACTGTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACA
 GCGTTATCTCTCCCAACCTCACTAA

1006758.120601

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCCHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFFVAILSTSFGSLEFGLPIPLSYVPV
FRSLITDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWLF
INSDFAFDFAFRLPLPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVVGIPVFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLT
LGT LWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTTCTGTCACACCCGTCACACACACATACCATGTT
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCTTGAAGCTCT
GGCTGCGACCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCCTAGAGAGGGC
AGACTATCAGGGTGCCCGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCAGA
AGACCGGGGCACTTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAGGCCAACTGGC
TACCAGGTCCCCACACAGTCCCGGGCTGCCCTTGGTTCTGTGTGCTTCTGGCCCTGGGGGCC
GGGTGGGCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCGTGGTGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCCACCCCTGGGC
GAGTGGCATTGTGCTCGGTCGGAAGCCACCACATGAGCCAGCAGGGGAAACCGGCAATGGC
ACCAAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCCTTGA
CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAATACT
CAAGTTTCTCTGGCTTCTCTATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCAAGAAT
CCAGCCCTGCACAACTTTCTTCTGCCCTCTCTTGCCCAAGAACAGCAGGCGAGGAGAGAG
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCAAGTTACC
CTCCAGCCACCTGCTGCATCTGTTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
AGAAGGAAGATCTGCACTACTTTGCGGCCCTGCTCCTCCGGTCCCCCACCCAGCTTCCT
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCCAG
ATGGACAAGCCTCAGCGTACCTGCAAGGCTTCTTCTGTGAGGAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAAGAAGTGAAGCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGGTGAAGGAAGGAGGGGTGATTG
TCTAGACTGAACATGGTACACATTTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCAATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAACTGCTCCAC
CTTTGAAGTTTGAACCTTAGTCCCTCCACACTCTGACTGCTGCCCTCCTCTCCCAAGCTCTC
TCACTGAGATTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTCTCTCTGAT
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTATTACCTGGGATTCATGATTCTTCTCT
CAGAGCTCTCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTTCTATCCGCTGTCCCAT
GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCACTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
TGTTTCAGAGGAAAAATAAATCAAACTGTATACTAAAATTAATAA

10006768.120601

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECILVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWFPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

10006768-120601

FIGURE 163

GCTGTTTTCTCTCGCGCCACCACTGGCCGCGGGCCGCAGCTCCAGGTGTCTAGCCGCCAGC
 CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGCAT
 GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCGCGGGGCCGTGACTGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCTACTCCGGGTCTGCGCGCGAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTCAGGAGGACCTGCGCTGTGCGCGAGGGGTCTGGGAGATGGGGCACT
 GGATCCAGCATCTCTCCGCCCTCCAGGACCTCTTCTGTGCACCTGGCTCAATAGGTCCAA
 GGTGAAAAGCAGCTACAGGTCATCTCAGTGCCTCAGTGGGTCTGTCTCTTCTTGTACTGG
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACCTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCCAAGAAAGGTGGCAGGAGGTGACA
 GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCCATCCAGCTGGTGA
 AGACACACAACCTGTGTGACCACCGAGAACTATATCTTTGGATACCAACCCCATGGTATCATG
 GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCACAGG
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCTGTGTGTAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTGAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGGTGCGGGCTGAGTCTCTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCTTGCAGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC
 GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCAGAAATACATTGGTTTCGCCCC
 ATGCATCTTCCATGGTCGAGGCCCTCTTCTCCTCCGACACCTGGGGGTGGTGCCCTACTCCA
 AGCCCATCACCCTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCAACCCAG
 CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA
 CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCTTGAGGTTGAAC**TGAG**CCAGCCTTCGGG
 GCCAATTCCTCGGAGGAACAGCTGCAAATCACTTTTTTGTCTGTAAATTTGGAAGTGTCA
 TGGGTGTCTGTGGGTTATTTAAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAA

1006763.120601

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRS
QWVRNWA VWR YFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPI TIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEV N

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

1006769-120601

FIGURE 165

GGGCGGCGGGATGGGGGCCGGGGCGGCGGGCGCCGCACTCGCTGAGGCCCCGACGACGAGGCCGGGCGGGGCCCA
 GGGCCGAGGAGCGCGCGGCCAGAGCGGGGCGCGGAGGCGACGCGGGGACGCCGCGGACGAGCAGGTGGCG
 GCGGCTGCAAGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCTTGGCA
 CGGCTGTCTCAGCGAGGGGCGTGCACCCGCTCCTGAGCAGCGCAATGGGCTGCTGGCTTCTCTGAAGACCCA
 GTTCGTGCTGCACTGCTGGTGGCTTGTCTTCTGGTGAGTGGTCTGTGATCAACTTGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCACTGCCGCTCGCTACTACTCTGGAGCCA
 ACTGGTCATGCTGCTGGATGGTGGTCTGCACGGAGTGTACACTGTTACGAGCAGGACGACGAGTAGAGCGCTT
 TGGGAAGGAGCAGCAGTCATCATCTCCAACACAACCTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA
 GCGCTTCGGAGTGCTGGGAGCTCCAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCTATCGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGAACCGTGGTGAAGGGCTGAG
 GCGCTGTCCGACTACCCGAGTACATGTGGTTCCTCTGTACTGCGAGGGGACGCGCTTACGCGAGACCAAGCA
 CCGCTTAGCATGGAGGTGGCGGCTGCTAAGGGCTCCTGTCTCCTCAAGTACCACTGCTGCCGCGACCAAGG
 CTTCAACACCGCAGTCAAGTGCCTCCGGGGGACAGTCGAGCTGTCTATGATGAACCTGAACTTCAGAGGAAA
 CAAGAACCCGTCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTCTCTCT
 GGAAGACATCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACCAGGAGAAGGACGCGCTCCA
 GGAATATATATAATCAGAAGGCGATGTTTCCAGGGGAGCAGTTAAGCCTGCCCGGAGGCGGTGGACCTCCTGAA
 CTTCTGCTCTGGGCCACCATCTCTCTGCTCCCTCTTCAGTTTGTCTTGGGCGTCTTGTCCAGCGGATCACC
 TCTCCTGATCCTGACTTCTTGGGGTTGTGGGAGCAGCTCCTTTGGAGTTCGAGAGTATGAGGAGAATCGCT
 TGAACCTGGGAGTGGAGATTGCAGTGAAGTGGATGATGATCTACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAACCAAGAAATCTGGAGTTGAAGTGTGTAGTTACTGACATGAAA
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGTGGTACCTTGAAGAT
 TTTCAAGGCTAATGAAAAAGAAATGAAGAAAATTAACAGCCTCAGAGACCATGGTGCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCAGAAAGGAGGAGAGAGAAAAGGTGAGAAAGAAATGCCCACAAAGCTGATGAAAAACA
 GTAACCTACCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCTAT
 AATCAAAGTGTCAAATGACAAAGAAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATCTTTG
 ATCAGATTAAACAGCTCATTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
 AACCTTCAAGTGAATTAATTTGACCTTTGAGTCTTAGATGGTCTGACCTTGTCTTCAAGGACAGTITTTCA
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTACCTGTAGGAAGGCGTGTCTTTAGGCCGGGACAGTGGC
 TTACACCTGTAATCCAGCAGCTTTGGAGGGCCAGACGGGTGGATCATTGGGGTCAGGCTGATCTCAAATCCT
 GAGTTCAGGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGACGGCGTGAGCCACTGCGCTGGCCGGA
 ATTTCTTTTAAAGCTGAATGATGGGGGCGGACGATGGCTCAGCCTGTGATCCCAAGTAGCTTGGATTGTA
 AACATGCACCACCATGCCTGGCTAATTTTGTATTTTGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCCTTGA
 GCATCTTGTGATGTCTTATTTGGCCATTGTATATCTTCTATCTCTTTGGGAAATGTCTGTTCAAGTCTTTG
 CTTTAAATTTTATTTATTTATTTATTTATTTTGTAGACAGGCTTGTCTGTGTTGCCAGGCTGGAGTA
 CAGTGGCAGCTGTGGCTCAGTCGAGCCTCGACCTCCTGGGCTCAGTGTGATCCTCCACCTGCTCCTCGATCTCCT
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
 TGCCAGGCTGGTCTTGAACCTCAGTCAAGTGTATCTGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAATCCCAAAATTAACACACACACACAAAAAACCACTGATTCAAATGGGCA
 GAGGGGCGGCTGTGGCCCAACTACAGGAGACTGAAGTGGGAGGATCGCTTGGCATGAGAAAGTCAGGCTG
 CAGTGAGTCGAGTTGTGCGACTGCATCCAGCTGGAACACAGAGTGAACCTGCTC

FIGURE 166

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRNLNCRAYSLSWSQLV
MLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTTLLN
FLSWATILLSPLFSFVLGVFASGSPLLLITFLGFGVGAASFGVRRLLIGESLEPGRWRLQ

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

1006768-120601

FIGURE 167

GATATTCTTTATTTTTTAAGAATCTGAAGTACT**TATG**CATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTGTTCC**TAA**TGTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACCTTCTCTACTTAATATGTAGTC
 ATCCTGCGAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTGTGTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCGAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCACATGTGGTGGGTGCT
 CATGTTTATAGAGCTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTTGATTCACTAGGCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGTTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

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 1006768.10604

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCF SFALALGHFLLISLVGKLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

10006768.120604

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTTAAATCTGTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTACGTCTGGAGGCACTGACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATT
 CATAGCGCATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCACTTCTCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAGGAACTTGTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAGGC
 ATCGAGTCTCCTGCATTCACTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTCTTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGCT
 TCAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGAAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

10006768.120601

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWFLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

1006763-12604

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCCGCCCATGACCCAGCCGGTGCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGGCTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCTCGCCGTCTCAGAGTCTGTGGCGCGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAAGGTCTACATCAGCCTCTTCCCCCTGGGCATGGACTCACCTTGGCCTTCAAGAT
 CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTCGAAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPPWRRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYVIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

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[illegible]

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAARAPRRGPLGGRKKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEKEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKSAKPKQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRKSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGEEELAGEEAPQEKAEDKPDSTDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCCTCGGACTCTTACCTTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATA
 ACACCAATTTGAAGAGGAACATTTGTTTCATCAGTAATGCTAATAAAGATGAAGACTTAAAGCCAGAAGCCAAG
 TTTTACCTTTTTCCTGGTTTGTAGTAGCTTAAGCATGACCATGTGTTCCTCCAGCTCACTGGGCACTTTGAAGCA
 AATATTCCAAGACTCAAGCTAACCTACAAGACTTGTGCTTCCAATAGCTGTATTCCCTTTTGGGTCTATC
 AGAAGGACTGGATTTCACACTCTTCTCTTAGATGAGGAAGAGGCGGCTCTCTTGGGAGCCAAAGCCACAT
 CTTTCTACTCAGCTCGGTTGACTTAAACAAAAATTTAAGAAGATTATTGGCCTGCTGCAAGGAACCGGGTGA
 ATTATATAAATTAGCTGGGAAAGATGCCAATACAGAATTGCAAAATTTATCAGAGTACTTGGCCCTATTAACA
 AACTCACATATATGTGTGGAACTGGAGCATTTATCCAAATATGTGGGTATATTGACTCTGGAGTCTACAAGGA
 GGTATATTATATCTCAAACTAGACACACATAATTTGGAGTCTGGCAGACTGAATGCTCCTTCCGATCTCAGCAGCC
 TTTTGTCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTCTCGATTTCCTTGGCAAGATACTGCAAT
 CACTCGATCCCTTGGGCTACTCATGACCACCACATACATCAGAAGCTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTGGAACCTTCTCATACAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTTCG
 TGAATCATCTCAAGAGGCGAGTACCTCCGATAAAACCATCTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAAGCAGCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGTGTTGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAAGAAGATCTGT
 AGTATATTGGAGTCTTTACTACAACAGCTCCATCTTCAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGACTTTTTAATGGTCCATATGCTCATAAGGAAGTGCAGACCATCGTTGGTGCAATGATGGGAGAAT
 TCCATTCCACGGGCTGCTACATGTCCAAGCAAAACCTATGACCCACTGATTAAAGTCCACCGAGATTTTCCAGA
 TGTATGCTCACTCAGTTTCTAAGCGGCGACTCTGTGTGATAAGTCCGATTAAGCCAGTCCAGGAGGACCAAGCT
 CAGAGAAGATCAATGTGGATTACAGACTGACACAGTAGTGGTGGATCATGTCTTTGCAAGAAGTGGCCAGTACGA
 TGTAAATTGTTCTTGGAAAGACATTTGGAAGCTGTCTCAAGTTGTGCAGACTTTCAAAGAAAGTGGAAATTGGA
 AGAGCTTAGTGTGGAGGAGTTCAGATATTTCAAGCACTCATCAATCATTTGAACATGGAAATTGTCTCTGAAGCA
 GCAACAATTGTACATGGTTCCCGAGATGGATTAGTTGAGCTCTCTGCCAGATGGCAGCACTTATGGGAAGC
 TTGCGCAGACTGTTGCTTGGCAGAGACCCCTACTGTGCTGGGATGGAATGCACTGCTCTCGATATGCTCTCAC
 CTTCTAAAGGAGAGCTAGACGCCAGAGTGAATAATGGCAGCCCAATCCCAAGTCTGGGCAATGGACAG
 CATTAGTCATGAATCTGCTGATTGAAAAGGTGATTTTGGCAATTGAATTTAACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAAGCAAGCACTATTAAATGGTATATCCAGAGGTCAGGCGATGAGCATCAGAGGAGTTGAAGCCGA
 TGAAGAATCATCAAAACGGAATATGGCTACTGATTCGAAGTTTGCAAGAAGAGGATTTGCGGATGTATTACTG
 CAAGGCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCAATTGAGAATGAACAGATTGGA
 AATACCCAGAGGGGCGAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCAAGGTTGAGATCAAGA
 CTACATCCAATTCCTTAGCAGCCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCAGAGGGAGAAGCG
 GAGACAGAGAAACAGGGGGGCCAAAGTGAAGACATGCAAGGAATGAAGAAGAAAGCAAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGCTAGTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAAACATTTGCTCTGTGTTTGTATATCCCTTATAGTAATTCATAAATGCTCCCATGGATTTTGTCTAAGG
 CACAAGACATAATCTGAATAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACCAAGTTT
 CCAAGAACAAATCTTGACAAGCAAGATATAAGAATTTATCTAAAAATAGGGGTTTACAGTTGAATAAGTTT
 TGTTTGTAGTTTGAATTTATTTGTCATGTAATAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGATATAAGT
 GCTTTATTCCTCGAATTGCCATTAAAGCATGGAATTTACCATGCAGTTGTGCTATGTCTTATGAACAGATATAT
 CATTTCTATTGAGAAGCAGCTACCTTTGTGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACTCCCATATC
 AACAGCAATTTCTCAGTGAAGCAATTCACCTCGGAGAAATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTTC
 TGGCCACTGGGTTAAATTTAGTGTACTACAACATGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTCT
 ATTGACTAGTCAGGAGTACAGGTTACAGAGAGAAGTTGGTGCTTAGTATTGTATTTCTTTAGAGTATATCTAA
 GCTCTACAGGACAGATGCTTAATTAATACTTTAATAAGATATGGGAAAATTTTAAATAAACAGGAAGAACAT
 TATGATGTAGATATGATCCTGCTGGAAGGCATGCAGATGGGATTGTAGAAGAGCAAGGAAGACAGGCAT
 AATTTCTGCTGTTGGGAAAACCTATATCCCATGAAAGGAAGAACAATCACAAATAAAGTGAGAGTAAATGTAA
 TGGAGCTCTTTTCACTAGGTAATAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATTATAACA
 AATGCTGCAAAATCTGAGGAACACATAAATCTTCTGAAGAATCATAGGAGAGTAGAGCATTTTATTTATAAC
 CAGTATATTTCAGTATATATTCTCTCTTTTAAAAAATATTATCATACTGTATATTCTTTCTTTACTGCT
 CTTTATCTCTCTGTATATTGGATTGTGATTATTTGAGTGAATAGGAAGAACATATTTAACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTGTTGAATACAGACAGATGATTAATTTAAC
 AACGGAAAGGCTTAAATTAACCTCTTGACATCTTCACTCAACCTTTTCTATTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTGTTTTGTAAATTAACAAATAAAGCCTGCTACATGT

10066768.120601

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQITLLLD EERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFFFRSSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVPYV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCC LARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECI PKSQQA
TIKWIYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

1006768-120601

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGACAGGTCATCCTGGAGCATGCCACC GCGGGGGAGCAGA
 CAACCTCCGAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGACCTGGTGTATTTCCCCACCCCCAC
 CTCAGACAGTTTCAGCCAGCAGAGGACTGATCAGGTGTGTGCTGGAGTGGGAGGACGAAGCGTGGCTGGCAAGA
 GTGGCTGGAGAAAGAGGTTTCAGCCGCTTGACCAGCCGAGCTGCCGCTGACTACAAGATCCAGAACCATGGGCAT
 GGGTGTAGGTGGGGGGCCAGAGGTGTCATGTGCACCTCTTTGCTCAGCAAGAAAGAGCTGAGAGGGGGATCTTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGGAGGGAAGGTATTTAAAGGTAAACAGTGTGGCACAATAGTTAA
 GAGCACAAGTTTTGAGCTAGACCAGACATAGGTTCAAAATCTCTTCTGTTGCTTCCATGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCTAAAGTAGGGCCCAATAATAGCAACCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGT**CATG**CAACTAGCAAAAGTACCGATCCCATAGTAAGTCTATGCCCCACAG
 TATTTCCACCCACCCCTGTTCTCTGCTTCCCACCCAGGTACTGCAACGACTGGAGCAGAGCGGCAGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAACTGCGAGAGAGCATCCGCGGGGACAGGTGAGCC
 AGGTGAAGGGGGCTGCCGGCTGCCCTGCTCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTCCCC
 CCCAAGCCCTGGCCACGAGSGCCCTCCCTGCCCTGCAACGCTGGTATTTCGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAAATCACGGAGGTTGAGTGGCTGGAGGTCATAGAGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGGAGGTTAGGCTTTGCTGCCCTGACGATATCTCAACTTCCCGGAACCTTCCCTCCACAGAGCAGCC
 AAGACAGTGACAATCTCCGCGGGCAGAGCCACAGCACTTCCGCGCACAGGCCCTGTACAGCTACACCGGACAGA
 GTGCAGAGAGCTGAGCTTCTGAGGGGCACTCATCCGTCTGCTGCCCGGGCCCAAGATGAGTATGATGAGC
 GCTTTGAGAGGGGAATTTGGGGGCCCTGTGGGGTCTTCCCTCCCTGCTGCTGAGGAAGAGCTTCTGGCCGCC
 CAGGGCCACTGACTCTGACCTCTGACCTGAAAGAGTCTGCGCTCCCTCTCTCCCTCAGCTTCTCCCTCCGAC
 CTACCTGTGTGTTGGATGGGCCCTTGCACCTGTCTGCTGCCGGGACAAAGCCCTGGACTTCCCTGGGTCTCTGG
 ACATGATGGCACTCTGACTCAGGCGGATGCTGCCACCACTTCCCGCCGCGTCAAGGACCCCGGATCTGGCCACC
 CAGATCCCCCTCAG**CTGA**AGCAGGGGAAGCCTTGACCCCAAGTGAATGCTGCTGCTTCCCTATCTCTCAAGCTGTAGA
 CCACACCATCAATGATCCAGAGCAACAGCCAAAGCTGGAATCGCCCTTATTTCCACACCTCACTTCCAAGGTT
 GGAAACTTGGCCCTTCCCAATTTTAGAGCTGGAAACCACTCTTTTTCCTTCAATTTGTTCTATCATCTCTAGGACC
 GGAACACTACTACTTCTCTCTGTCATGACCTTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAACC
 ATCCATCAAGTCTCTAGTAGTTCTGGCCCACTCTTCCCAACCTGGCTCCATGACCAACCCCACTCTGGATG
 CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAAATGAATAAGGGCACGAAGGCCAGGCCAGGGCTGGGCCTCTTGTG
 CTAAGAGGGCAGGGGGCTACGGTGTATTGCTTTAGGGGCCCAACACGGGCAGGGGGCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCAGGTGTTGGGGAAGCGGGGACGGCAGCTGTTGCAAGGCAGGGGAAGGAGAAGAC
 TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGTGTCCT
 AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTCACGCCCAACCAACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCACAATGAAGGAGACTTGAGAAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
 TTTTCCCTCGGGCTCCAGGACCTTCCCTACCTCCACCAACCAACCAAGGGATTATAGCAAAAGGCTTAAGCTGC
 AGTTTACTCTGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGTGATGGGAAGATGAGATTAACTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACTGAGAGAAAGGGGAGGGG
 TCAACAATGAGAGACCAGGATAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAGAGCCACAGCCAGCTGC
 AGTCCCGGCTGTGTTTTCCTACTGCTGATCAGAAGTGTCTGGTGTGCTTGGCTGCCATTGGCTCTTGAAGTGC
 GCAGCCCTGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAGCTCTGGGGTTCCTTCAAGTG
 CACGAGGGTTAGGCTGTGCTTCCCTGAGTCTCTCATCTGTAAGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
 TCTCAGGGGGAGCCTCTCCATGGCAGGCATCCCTGCTTGGGCTGCCCTCCCCAGACCCCTGACCAACCCCT
 GGTCTGTCCCCACAGAGCCAGCTCCTGCTGTGTTGGGGAGGCCATCAGGCTGTCTGTGAGTCTCATAGGCT
 TCTCAATGTGTGTCACCCGAAGATCGGGAGGGGAGGAACACTGGGCTTAAAGCACAACACTCAGAGGCTGCTTG
 GCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGTACTTCCCTTGGCTTAAAGTAGGGGAGGCTTCTC
 AGATTGTGGGGCACTATGTGAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAGGGCCCACTT
 TTGGATCAGGTGCTGATGACTGGGCCCTTCCCTCAGCCCTTCCCTGGAGCAGCTGCCACCTGCCCA
 CAGAGAACAAGTGGTCTCCCTCTGCGGGGGCGGCTTTTCTCTCTTGGAGCTGCTGCTGACGCAAGTGGAG
 GCCTTCTGCTGCCGCTGAATGGATGCAAGGGCTCAGAGCCAGTGTGATGTGATGGAGGGGCTC
 CGTCTGCAAGCTGGAGGTGGCATCCACTGCACAGCAGGAGGAGGGAGCTGAGGGTAACTATTTCCATTTCCCT
 TCAATGTTTGTCTTACGTTCTTACGATGCTCTTAAACCCCAAGCCCCAATTTCCCAGGCCCAATTT

10086758.120601

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPFPVLCLFNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAQALATRALPCPAHVVFQAGREDELTITTEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPSSQSDNPNCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

1006768-120601

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAAAGCGGCCACAGAGTCTCTACAGAGGGAGAGGCCACAGAGAGCTGCAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGCTCAGGAGGAGAGTTTGGAGAGGCCAGACCCCTGG
 GCGACTCTCTCCAAGGCCAAGGACTAAGTTTTCTCATTTTCTTAAAGCGTCTCAGCCCTCTCGAAACTTTTGG
 TCTGACCTTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCTTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCACTGCCATGCTCCAGAGAGGCTCGCATCCCGGGAGGGG
 CTGGCAGGGGCGTGGCTGTGGGAGCCCAACCTGCTGCTCTGCTCCCATTTGCGCGTCTCTGCGTGGTGTG
 CTGTGTTCTGCTACTGCTGGCCTCTCTCTGCCCTCAGCCCGGCTGGCAGGCCCTCCCGGGAGGAGGAGAT
 CGTGTCTCAGAGAGATCAACGGCAGCGTCTGCTGCTGGCTCGGGCCCTCGCAGGCTGTTGTCGCGCTTGA
 GGCCTTTGGGAGAGCCTGCTACTAGAGCTGGAGCAGGACTCGCGTGTGCAAGGTCGAGGGGCTGACAGTGCAGTA
 CTTGGGGCCAGGCGCCTGAGCTGCTGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCCACATCAATGGAGATCC
 GGAGTCGTTGGCATCTCTGCACTGGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACCTCA
 CTTCCAGCCCTGGAGGAGGACCCCTAAGTCTGCTGGGGAGCCTGGGGCTCACATCTACGCCGGAAGAGTCC
 TGGCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTGGAAGCCCCAGCCCCAGACCCGGAAGAGCCAA
 GCCTTTTCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAAGTGGCCGCTTCCACGGTGC
 GGGGCTAAAGCGCTACTGCTAAGACTGATGGCAGCAGCAGCCAGGCGCTTCAAGCACCCAAAGCATCCGAATCC
 TGTGAGCTTGGTGGTGACTCGGCTAGTGATCTGGGGTCAGGCAGGAGGGGCCCAAGTGGGGCCACTGCTGCG
 CCAGAGCTCGCGACAGTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTGGGCTGACCATCTTGA
 CACAGCCANTTCTGTTTACCCTCAGGACCTGTGTGGAGTCTCCACTTGGCAGACGCTGGGCTGCTGATGTGG
 CACCGTCTGTGACCCGCTCGGAGCTGTGCCATTTGTGGAGGATGATGGGCTCAGTCAAGCTTCTACTGCTGCTCA
 TGAACCTGGGCTGCTTCAACATGCTCCATGACAACTCAAGCATGCATCAGTTTGAATGGGCTTGTGACAGC
 CTCTCGGCATCTCATGSCCCTGTGATGGCTCATGTGGATCTTGAGGAGGCTGCTGCTCCCTGCACTGGCCGCTT
 CACTCATGACTTCTTGACAAATGGCTATGGGCATGCTCTTAGCAACACAGAGGCTCATTTGCATCTGCTGCTGT
 GACTTCTCTCGGAGGACATGATGCTGACCGCAGTGCCAGCTGACCTTGGGCCGAGCTGGCCATTTGCTCC
 ACAGCTGCCCGCCCTCTGTGCTGACCTCTGGTGTCTGGCCACCTCAATGGCCATGCATGTGCCAGACCAAAAC
 CTGCGCTGGGCCGATGGCAGCCCTCGCGGCCGCCACAGGCTGCACTGGGTGGTCTGCTGCTGCGAGGACCA
 GCTCCAGGACTTCAATATTCAACAGGCTGGTGGTGGGGTCTTGGGAGACATGGGGTGTGCTGCTCGGACCTG
 TGGGGTGGTGTGAGTCTCTCCCGGAGACTGCACGAGGCTGCTCCCGGGAATGGGCAAGTACTGTGAGGG
 CGCGGTAACCGCTTCCGCTCTGCAACACTGAGGAGTGCACCACTGGCTGACCTGACCTTCCGCGAGGAGCA
 GTGTGCTGCTCAACACCCAGCGACCGCTCTTCAAGAGCTTCCAGGGCCATGGATGGGTTCTCGCTACAC
 AGGCGTGGCCCCCAGGACCGATGCAAACTCACTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
 ACGGTTGGTAGATGGGAGCCCTGTTCCCGGAGAGCTCCTCGGTCTGTGTCCAGGGCCATGCATCCATCGTG
 CTGTGATCGCATCTTGGCTCCAAGAGAAGTTTGACAAGTGATGGTGTGCGGAGGGGACGGTTCTGTTGACAG
 CAAGCAGTCAGCATCTCTCAGGAATTCAGGTACGGATACAACAATGTGGTCACTACTCCCGCGGGGGCCACCA
 CATTTCTTGGCGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGGCCCTAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGGCAGTCAGCTTGGCGTA
 CAGCGGGGCCACTGCAGCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGGCTTTGACACTGCAAGTCTCT
 AGTGGCTGGCAACCCCGGACACAGCCTCCGATACAGCTTCTTGTGCCCCGGCCGACCCCTTCAACGCCACG
 CCAACTCCCGAGGACTGGCTGCACCGAAGACAGATCTGGAGATCCTTGGCGCGCGCCCTGGGCGGGCAG
 GAAATTAACCTCACTATCCCGGCTGCCCTTCTGGGCACCGGGGCTCGGACTTGGTGGGAGAAAGAGAGAGCTT
 CTGTGCTGCTCATGTCTAAGACTCAGTGGGAGGGGCTGTGGCGTGAAGACTGCCCTCCTCTCTGCGCTAAT
 GCGAGGCTGGCCCTGCCCTGCTTCTGCTGGAGGCAAGTATGGGTTAGTGGATGGAAGGGGCTGACAGAC
 AGCCCTCCATCTAACTGCCCTCTGCGCTCGGGTCAAGAGGGAGGGGGAAGCAGGGAGGGCTGGGGCC
 GCTGTATGCTTTATTTAGTATTTATTTACTTTATTTAGCACAGGGAAGGGAAGGACTAGGCTAGGCTTCTGGGAA
 CCTGACCCCTGACCCCTGAGCCCTCACCCTGGGGCTAGGAAATCAGGGTGGTGTGATAGGTATAGTGGTGTG
 TGTGTATCGGTGTGTGTGTGTGTGAAATGTGTGTGCTTATGATGATCAACCTTCTGTCTTCTTCTCT
 TTCTGATTTTATTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCTCAGGGAGTAGGGATATCTTTT
 TTTTCTTTCTTTCTTTCTTTCTTTCTTTTGGACAGATCTGCTGCTGCGCCAGGCTGGAGTGCATG
 GCACATCTCGGCTCACTGCATCTCCGCTCCCGGCTCAAGTGAATCTCATGCTCAGGCTCCTGACTAGCTG
 GATTAAGGCTCCTGCCACCCCGCCAGCTAATTTTGTGTTGTTTGGACAGAGTCTGCTGATTTGCTTCTTCT
 ACCAGGGCTGGAATGTTTCACTCACTGCAACCTTGGCAGCTGGGTTCAGCAATCTCTGCTGCTGAGCTCC
 CGATAGCTGAGATTATAGGCCACTACACACCGCCCGCTAATTTTGTATTTTATGATGAGAGCGGGGTTCAC
 CATGTTGGCCAGGCTGGTCTGCAACTCTGACCTTAGGTGATCCACTCGCTCATCTCCAAAGTGGTGGGAT
 ACAGGCGTAGGACACGCTGCTGGCCAGCCCAACTAATTTTGTATTTTATGATGAGAGCAGGGTTTCAACATG
 TGGCCAGGCTGCTTGTGAATCTCTGACCTCAGGTAAATGACCTGCTCGGCTCCCAAGTGTGGGATACAGG
 TGTGAGCCACCAGCCCGGTACATATTTTAAATTTGAATTTACTATTATGTGATCCTTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTTCTCATTGCCAATAATAATACCTCCCTTAGAAG
TTTGTTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

1006768-120601

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGLAGRWLGAQPCLLLPVPLSWLVWLLLLLASLPASPLPREEEIV
FPEKLNQSVLPQSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQGAPELLGGAEP
GTYLTGTINGDPESVASLHWDGALLGLVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPNCNVKALPGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA
AAKAFKHPSIRNPVSLVVTIRLVILGSGEEGPQVGPSSAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDFPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAVPMHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCLTFGPDSTRHCPQLPPCAALWC SGHLNNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLEHMDQLQDENIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLKFSFPGPMDWVPRYTGVAPODQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYALAKLPDGSYALNGEYTL
MPSPTDVLPGAVSLRYSGATAASETLSGHGFLAQPLTLQVLVAGNPQDTRLRYSFVPRPT
PSTPRPTPDWLHRRQAILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

10006768.120601

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
 AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATCCAAAATCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGCTTCCAATAAATGACTATACATG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTATTGTTGTATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

1006768.120601

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTTFFEQSVIWWPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRNRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

1006768-120301

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCA**ATG**GCCAGCAGCGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAACACCGCACCTGCCTACCAGCCACCACTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGCTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

10006763-120601
 10006763-120601

FIGURE 184

MASTAVQLLGFLLSFLGMVGLTITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSCMKFEIGQALYLGFISSSLSIGGTLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAFSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

1006768-120691

FIGURE 185

GAGCTCCCCTCAGGAGCGCTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTT**CAGGCTT**CACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGTGTCAGGCAGTGCAGAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTT**CAGACCAGGTACACATTTGGT**CGCGCTCTGTTCGTG
 GGCTGGTGCCTGGAGGCTCACACTAATTGGGGTGTGATGATGTGCATCGCTGCCGGGG
 CCTGGCACCAGAAGAAACCACTACAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTGT
 CCTACAAGCTCGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTCTCTCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCAAGAAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTT**GAGGCAACCAACCTTTCTACTG**
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTCTTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGCTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
 TTAAGTCCTAAATATAGTTAAATAAAATATGTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAGGAAATGAAAAATAAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATCTTTAA

10066768.120601

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

1006768-120601-10021-8929001

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG
 GAGTCCAGCTGGCTAAAACTCATCCAGAGGATAATGGAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTCCGCCCTTCATTGAAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGC AAAATCTATGATTCCTGCTGG
 CTCCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAACCAATGCTTTGATTGTTCTAGAAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACTTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA
 AGATTAATAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTTAGCTTAGGAGTTAGAAATCCTAACTTCTTTATCCCTTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTGTGATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGTTTTTCATTGTGTTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCGTGAAAAATAAATTTCTTTCTGTACCATTTCTGTTTAGTTTTACTAAA
 ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGTGCTTTATACATTTATA
 TTAATAAATTGTACATTTTTCTAATT

1006758.120601

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSSLALSPDLQAAGRLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

1006768-120601

FIGURE 189

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGCGCTTGTCTGGTCTACCTTGTCTGGGC
 CAAGTGTAACCACTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCACTCTTGGA
 TTGTCTTTGTATCTCAGGGGTCTTGACGCTAATCCCCGTGTCTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCCT
 CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGGTGGGGGGTGTCTGTCTGCACTT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT
 GCCATCTCTCGGGGGCCCTCTGAGTACCTACCAAGAATTACGCT**CTGA**CGTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
 CGTACCTTTTGTCTCTGCCTCCTGCTATTTTCTTTTGAAGTGAAGATATTTAAATTCATTT
 GAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTACCCCTGG
 ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
 CAGTCAAGCTATGGAAGTAAATGCGGAGGCTGCTTGTGTCTGGCTTTGCAACAAGACAGAC
 TGTCCCCAAGAGTTCTGTCTGCTGCTGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGACTGCCACCTCCGGAAGTCTGACCTCTGTTTCTCCGTCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTTATCAAATAAGCATG
 TTTTGTAGTGCA

1006768.12604

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGQPSHYMARYSTSAPAIRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

1006768-120604

FIGURE 191

GCCAAGGAGAACATCATCAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
 TTGCCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGACTCTGCCACAACCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGTCTCCTTGTGGCTCTCCCGCTGCCCCTGGAAACAGCCCAGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCCCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTGTACTGGTGGTAGG
 AATGAAAATGACTTACTTGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCAATCGCTGCTCCAATTTTCATATTCTAAATTCAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

1006768.126601

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

10006768-120504

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATG**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
AGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAATAATCTCCAGA

1006768-12661

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSSEASLSPKKVDCSIYKKYPVVAIPCFITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

1006768.120601

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
 CGCCGCC**ATGG**GCTGCCTCCCCGCGCGGCTGCTGTCTTGGCCCTGACCGGGCTGGCGCTGC
 TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
 AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTGATGAGAATAAAGCCAAAGA
 ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
 AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
 ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
 CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
 TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTTC
 TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
 CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAATGCCTTT
 TGATATTTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

1006768-120601

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNLKLMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDIYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

1006676.120604

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCTTTTCTCGGTGCTTGCTGCCTTCTGGTGTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCACTGCCCCAGCCGTAGGGACCCCAACGCCATCCAGCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCGAGCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTCACAGCAACACCGCCAG
CCCCGGACTCCCCGCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAG**TGCCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTC
GGACCTTGCTCCCCGCGCGCGGGGAGCTGCTGCGTCCCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCGCGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTGCTGCTCGCTCGGCCCCGGGCAGAGCCG
GGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTCCCCGGAACCCGTGCAGATTAAAGTAAGTGTGAAGTTTTAAAAAAAAA
AAAAAAA

1006763.120601

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEFSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPNNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

10066768.120601

FIGURE 199

GAGATTGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
 TCAGCTGCACCTCCTCCCCTCCAAGCATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
 TTGTGTCCGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAACAGGGTGCGGGTGACCCGTGG
 AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCCTTTCCTACTGCCTCCA
 CTTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
 TGGTTTTCTTGGCTTCTCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
 TTGTAACTGAGGACCACAATAAGAAATCTTTATATTTATCG

1006768..120501

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCBVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

1006768-120601

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGGAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAAACGGGGTAAGGGGAGGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCCTGACACCGC
 TGTTGGCAATGTCAAGACAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCAATTGGCAAGTTCTAGCAACATGCTCCTTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGCGGATGT
 TGCACCTCCCCACCACACCTGACACGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGCCAGAAAGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTTGGACCCAC
 GTGGCCTCCAGGAGGCAGTGTGCCCGCATCCCCCTCCAGAGGGCTGTGCCCGAGGTGCGG
 CACCCACTGTCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGCGCTTCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGGCACCAGGCTGGCTGGAGCCCTCCTCAGCAGAAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA
 TTACCCCTCAAAGGACCTGACAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTCTGCGAGGTGGTGAACCTCGAACCTGTCTTCAAGGCTGGCTCTGTGGT
 GCTCTGTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT
 TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGCATTGTCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACGTGCAAGGAGACTGGGTGTCTGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCCCAGTTTCTCTGGA
 GCTCCACAACACTGGACTTGGGCTGTGTGCAGACTGCCAGGCAGAAAGGGGACATCCTGGGCT
 GTCCCATGGTGTGGCTCCTTGACAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCGC
 AGGAAGGAGATTACCTTTGGCAGCCACAGCACCTGTGCTTGTCTGAGCAGGAGCAGGT
 GATTCTTCAAGACTGCACGGAGGAAGGCTTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTTCTTGGGAAATGCATGGAAGCTGGTGTCAAGAAAAAC
 AATAAAGATTGTACTGCTCCGTGCTGTGATGGAAGAAAGCCGACAGTGGCGCATTTGACCA
 GATAAATGCTGTGGATGAACGATGATGTCATGTCAAGGAAAAAGAGAAATTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCATGAAAGATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

10006768.120601

FIGURE 202

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTVAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYESPLEGLPPFISLREDQLLVAVALPOARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEEDGEVESEEEELTPFSLDPRGLQEALSARIPLQRALFEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQQLKSALSEYVAR
LEGVKLLRSNKRGLAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVS
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSEVILPCSRVGHYQNDSHSPLDQEATL
RNRVRIAETWLGSGFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMVLAPCSDSRQQQYLYQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWDFFQENGMIHVHILSGKCEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

100676.120601

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCTCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAAGCCACAGCCAGCCAGCC
 CGCCCCCCTGTGTCAGGGGAGGCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCTCTGCCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGACTATGTTTTGACGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTCGCGCCATTCT
 CTGTTCTGGGGGCCGTGGGGAAGGTGTGGACCCCAAGCTCTATGTGCACAAATACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTCGGGGACTCACCTACCCCAACCC
 TGACCATGAGGAGCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCAGTTGAACCGGTGAGGGGAGGGGCAATGGATGGGAGGGCAAGAGGGGAAGGCAAC
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCAGGCCCTGGCCCTCCCAAGGGGGCTGGACCAAGCTCCTCTCTGGGAGGCACCTTCT
 CTTCTCCAGTCTCTCAGGATCTGTGTCCATTCTCTGCTGCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTTCTCATGCCACCTTGCTAAGACAACCTCGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACATTCCCTTCTATCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACCAACCCGGAACACTCCCCAGCC
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGACACTCACTCCACCTCAC
 AGGCCATTGACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTTGACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
 TGTGCGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACTCGTTTCCGAGCCCTGCG
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTGATGG
 TCTCGTCCCAATCCACCACTTTGTTTCTCTGTCTCCCACTCACTCCAAGGATGCCGGGA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGGCCAGACTTCAACCCAGCCCA
 CTGCTAAATCTGTTTTCTGCAGATGGGTTTTGGGGAGTCGCCCTGCTGCACATACATGAGAA
 AGGGACTCCCAATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTGTCTGCTCGGCTG
 TCTGTGTGTGTCACATTCTTGACTTCAGAGCCCTCGAGCCCTCTCCCTTCCAGCCT
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCCTCAAGTCTACCTTCCCTTCCCGGACTCCCTCCTGTCCCTCCTTTT
 CCTCCCTCCTTCCACTCTCCTTCTCTTTTGGCTCCCTGCCCCTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTGTATTATCTCTTTCTCTCTCTGCTGATCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

1006768.120601

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGFAASFPQRLRGLLLLLLLQLPAPSSASEIPKGGKQAQLRQREVVDLYNGMCLQGPGAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEATIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

100076393-100076393

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGC**ATG**G
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

10066768.120601

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

1006768-120601

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCTCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC
CCAGAGGCGCTGGGAGTGTGGCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCTCCGGGCCATGGACACACATACATAAAACCAGGCCGCAT
CGACTGTGACGACCGCTGTGGCATCTTCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCAGCTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCCTCCAC
CTGGCTGTGTCATCGGGTAGGGCGGGGCCGTGGGTTGAGGGCGCACCACTTCCAAGCCTGTGT
CCACAGGTCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGCGACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGGCGGCTGCAGTCTTTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCTAAAGGTCCCCATAGGCTGTGGTTCC
ACCCCATCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGAGGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCATGCAGGTGGGGCTCTCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCCGGGCTGCACACCTTCGGACATCCAGGC
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACAGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGACAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

10006768.120601

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLF

Signal peptide:

amino acids 1-15

10066768.120601

FIGURE 209

AGCAGGAGCAGGAGAGGGACAA**ATG**GGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAATTTCCAGGCGTGTCATTTGGGATCAGCACTGATTCAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGTGACTGTGATTGGGTATTCAACAGCG
 TAATTCAGATTTCATCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCGCCAAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCTAAGTGGAATAATGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTTGAACTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACATAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGCGACGTGCACACACGCGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCTCTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCAAT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGTCTTTTTAAGGTTACCTAAGGGT
 TGAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAACCAAGG
 ATGGTTTTAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

1006753.120501

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAEFIAATEVAVIG
FFQDLEIPAVFILHSMVQKFPGVVSFGISTDSEVLTHYNITGNTICLFRLDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVSEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

1006768.120601

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCTGTAGAAAAAGAGAAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTATAGAAGGAAA
 AACTCTAACCGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTCTCTGGATCTCACC
 AGGGCCCACTCATATATGCACAGTTAGACCACTCCGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAAGATGTGT
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
 TGAAAAGATGGTATGATTCTAATATGTACCATTTGTCTTGCTGTTTTGTACTTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTAGAAAACATTCCTTTCCACATCATTTAGAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
 AAATGTGTCATATCAATTTCTGGATTATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCATTCTATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

1006768.120601

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIE
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

1006768-120604

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCGCGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCGGCCACAGGAGCAGTCCCTCGCCCCGTGCTCTCCGACAGCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGCATAGTGGTTGAGTTTCTGTAGATGGAAGAAAGTCT
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAGAGAAATGTTGCATTTGAGCAAGAAAAAGAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTAAAAATTC AATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTTAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAAA

1006768.120601

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEYGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMITTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGCGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCGGACACAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCAAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATCACTGCTCACTTGATACGTTATTTCAGAAACCCAG
 GAAATGGCTGTCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

1006768.120601

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPIRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

1006768-120691

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGAGCAGGTGCTCCGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGTCTTTGTAGGCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCTTAC
 CTCTATAAATCTACCAGCATTACTTCTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAATCTCTT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGTCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCTTGGCCCTTCGAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCCTCCTGTCGGACCGCCGC
 GTGCTGCTGCTGGGCACCATACAAGCTCTATTTGAGAGTGTATCTTTCATCTTTGTCTTCCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGTTAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGTG
 GACTGACTTTGTGACTGTCCTGTGGTTTCTCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAACACTTTTAAATGATCAAAAAAAAAA

1006768.126601

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFVNNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSTRCAGGLRCLLSDRR
VLLLTGTIQLFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFISCSAVMMALLAVVGLFTVVRHDA
ELRVSPSTEOPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGGCGCGGGCCGGGCCCTGGAG**ATC**
 GTCCCGGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACGATACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCAACGACATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAG**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAACAACAAAGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTGG
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1006768.120601
 1006768.120601

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

10006768.120601

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCCTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCCTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAAATGGCTGTGTTTAAATGTGATCTATCTGGAAAATGAGGACTC
CGAA**TAAAA**AGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

10036768.12601

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

10005763-120601

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTGAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTGCGT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

1006768.120601

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

1006758-120601

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACCTGGGGTCTCATCAGGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAAATTGCCTGGAAGAAATACATCATGTTTTTCGATAAGAGAATTTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTGTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTTCTGCGGTGTGAGCGAGCCCTGACTCACTACAGTGACGCTG
 ACAGGGGCTGTGATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCCACTGTCTTACTGACAACTGCTTCTTCTGCGGAAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAACTTAAGTATAAT
 CAATTTAAAGGGCTCAACCACTCACCTGGCTATACCTTGACCAATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCCTTAGTTCCAATAGAA
 TCTCCTATTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTTCTTGGGATCTGAACAGTTTCGGGGCTTCGCGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCCTGAGAACCATCCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCCTTACTTGCAGTGGAAATAAAATCAGTGTCCATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTATCTGTCCAGCTCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAATACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCAAGCTCCCCAGGCCAAGCAT
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCTGCTGGTTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTTAAAGCAAT
 GACTCCCAGCCAGGAATTTTATGTAGATTATAAACCCACCAACGAGGAGACCGGAGA
 TGCTGCTGAATGGGACGGGACCTGCGACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACCT
 TGGTGCATATCAAGGGAACGGGATGCCCCCCCTCCCTTCCCTCCTCCTCCTTTGGTG
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTCTAATACTGGTCATTTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAACATCAATGTGAAGCTTGAACCTCCGGTTAATATA
 TACCTATTGTATAAGACCTTTACTGATTCATTAAATGTGCGATTGTTTTAAAGATAAACT
 CTTTTCATAGGTAAAAAATAA

1006758.120601

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVVFAGMIRKELHLEHNQF SKLNLALFPRLVSLQNLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

1006758.120601

FIGURE 227

AGTTCCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAATATGCTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTGTTGCCGCTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACGTGTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGAGATTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

1006768.120604

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

10006768-120601

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGAGCGCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGCGCTCAGAAGCTCCGTGGCGGCGGCACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAAATATACAATATTGAGGATATTTTTTCTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTCTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAACTACTAGACTTAAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTGTGTGCCAGTAA
 CCACAAATAAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTTGTCTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGTGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTCT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCAATTTGTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA
 AGGTTAATTATTGTATATTTTTAAAAATTACACTTATAAGAGTATAATCTTGAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT
 GTAAACTCTAATCTTATCTTATTGGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTCACATACATGAATGTTCAATTTAAAGTTTAACTCTTTGAGTGTCT
 ATGCTATCAGGAAGCACATTTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAAA
 GGTACTTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAATTTGTATAACAGATGCATTAGATATTCAATTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTGGGTAATTTCTAGTATAAAAACAAATTACTTTTAT
 TTAATTTCCCTTGTAGCAAACTCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTTAT
 CTCTATAGTAACTGCTTAACTGAGCTAGCTTCTAGATTTAGACTATATAGAAATTTAGATAT
 TGTATTGTTCTGCTATTATAATATGCTACCCACATGTAGCAATAATTACAATATTTTATTAATA
 TAAATATGTGAATATTGTTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

10006768.120601

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:**Signal peptide:**

amino acids 1-26

1006768.120604

FIGURE 231

CGCGGCGGGGCGCGGGGGTGAAGCTGCCGAGGCGGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATCCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCCAGACAAACCGGCCATGCT
TCCCGGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCAGACGCTTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGTGCCATCCCTCTGGACACAGCCCA
CTTGGACCTGTCTCCAAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGCT
ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCC
TTCTCCCGCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCTGACAGCCTGCC
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
AGGTCTCAGTGTCTGCCCTCACGACGCACAGTCAGGGCCGGGCATACACGTGGACCTCTCC
CACAACTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCTGCTGCGCCCACT
TCAGAGCCTGAACCTGGCTTGAACCGGCTCCATGCGGTGCCAACCTCCGAGACTTGCCCC
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCTTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTGTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
TGGCTTCGCTGAGCTACCGGGCTCGCAGGTCTCGGACCTGTGCGGCAACCCCAAGCTTAAT
GGGCAGGAGCTGAGGTGTTTTCAGGCCTGAGCTCCCTGACAGGAGCTGGACCTTTCGGGCACC
AACTTGGTGCCCTGCTGAGGCGCTGCTCTCCACCTCCCGGCATCGAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCGCTGGTGCGGGAGGGACCTACCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGGCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
ATCTTG**TGA**CAATGTGTGGGCCAGGGCCACATAACAGACTGCTGTCCTGGCTGCCTGAGC
GTCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGAGGCCGAGGCCTATGTGGCA
GCGTCACACAGGAGTTGTGGGCTTAGGAGAGGCTTTGGACCTGGGAGGCCACCTAGGAGC
AAAGTCTCACCCTTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGAATTCGATGCCA
AACCAGACTCGGGTCCCTCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCTTCCCTCAT
GCCTGGGCGGCTGACCCGCAATGGGAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
GTTACGTTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTTCTAT
TTCCTTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCTCTCTCATGTGAC
AGATGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
ATGACTGGAGCACAGCCTCTGCTCCCGAGCCCGGACCCATGCACTTTCTTGTCTCCTCTA
ATAAGCCCCACCTCCCCGCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
CCAGCTTAGCCATTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGATGGAAACCTACC
CATTTTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCCTCA
TCTGCTGGGATCTCCAAGGGGCTCTGGATTCACTCCCCAGTGGCCCTGAGCAGCAGCAGC
CCTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCATGTCTATGC
TCTACCCCGAGGCGAGCATCTCAGCTTCCGAACCCCTGGGCTGTTTCTTAGTCTTCATTTTA
TAAAGTTGTTGCTTTTAAACGGAGTGTCACTTTCAACCGGCTCCCTACCCCTGCTGGC
CGGGATGGAGACATGTATTGTAAAGCAGAAAGGTTGCATTTGTTCACTTTTGTATAT
ATTGTCCTGGGCTGTGTTGGGTTGGGGGAAGCTGGGCATAGTGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGCTTCCCCACCTGCTAGC
CCATCATCTATCTAACCGGTCTTGATTAAATAAACACTATAAAGGTTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVLDLSHNLHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

1006768.120601

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCCTCCAGTTCCTCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGCT
 GTTCCAGGCTTACCTGCTGGGCTAAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTGAGGCTTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAAGCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGCTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGATCTTATTTATGCATTACTTGCTTCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
 ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGGTTATTCAATTGTATCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATGAAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTATGTGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTTGTGTAT
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

1006768.120601

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261.aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKDKDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAQAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

1006768.120601

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTTCAGATGCAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGTTACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT
 ATTGAATACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT
 TCAAGGTGAAGGATTTCATGAGTCTATATAAAGGCTTTTTACCATCTTGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

1006768.121601

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVYRTALGIIIEEGFLKLWQGVTPAIYRHHVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

10005758.120601

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
 TTAAGAAGTAAAA**ATGC**CAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGAC**TC**AGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTACATTTTTATGTTT
 TGAGTTTGAATAGTTTTATGAAATTCCTTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCAATTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
 AAAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTCTAGCCTGGGGGAGAAAGTAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTGGTAAAGA
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

1006768.120601

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

10006768.120601

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTCACTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCTTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTATTATCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACCTACTTTGCGTTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCCTGGTGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGTGCTTTCTGTGAGGG
 ACTGTGACGGTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAATTTTA
 TTTTGTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAA

10006768.120601

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMFSMTIRLPRWLAASPTKEIQVKKYKGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKFLSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTN KYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

1000768-1000768

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGCACCCCTTCCTGGGACACT**TATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTAGACAGACAGTGT
 GACATTTGACCTGATTTGCCTGCTCTGCAGCCACGGATATGACCAGCCTGGCACCAGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCACCTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCATGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCGATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA
 TCCTCGTATACCAGAGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTTATTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCAT**TAA**ATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTGTTAATGCAGAGANCAAATCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCCTTACCCCTCACTTTTATGGCCCTTCCCTTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTGTCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTTGAAATTAAGTTTCTGACTTT

100676-126674

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ
INSEATFAELHIVHYDSDSYSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
FSTEEEPSKLLVQNYRALQPLNQRMVFAFIQAGSSYTTGEMLSLGVGILVGCCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

1006768-120631
120621-8976001

FIGURE 243

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
 GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTAGCATTCTACTGTTTTGTCTTCTAGG
 ATCAACTCGGTTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC
 CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
 ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
 AATGACACCTGGTACCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC
 TGCACCCACATGTGTTACCAATTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGC
 TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCTTGTTCCTCCGGGAGGCAT
 CCTGCCACCAGCTCAGGCAGGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG
 GAGCAGGTGTAATCCTGCCACCCAGGGAACCCAGCAGGCCGCTCCCAACTCCCAGTGGC
 ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
 GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAAGCTGTTCAAATTTTTTCAACTAAG
 CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA
 GACACATTGGATAGTCTTAGAAGAAATTAATTCCTTAATTTACCTGAAAATATTCTTGAAATT
 TCAGAAAAATATGTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATCAATGGATAAAT
 CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAACATATTGGA
 ACTGGAAA
 AAAAAAAAAAAAAAAAAA

1006768-120601

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFIVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

10066768-120601

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCCATGCGACCCAGGGCCCCGCCCTCCCCGAGCGGCTCCGCGGCTCC
 TGCTGCTCTGCTGCTGCAGCTGCCCCGCGCGTCGAGCGCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGCGAGAGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTTCACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTGGACCAAGGAAG
 CCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCCAAATA
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTTCATTTTGCTTCAATCAAAGT
 GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTTGTAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

1006768.120601

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

1006763-120601